

MATCH WITH FIG. 1A

241	AAGCTATTCTCTTTCACCAAGTACTTTCTCAAGATTGAGAAGAACGGGAAGGTCAGCGGG	300
	-----+-----+-----+-----+-----+-----+-----+	
	TTCGATAAGAGAAAGTGGTTCATGAAAGAGTTCTAACTCTTCTTGCCCTTCCAGTCGCCC	
	K L F S F T K Y F L K I E K N G K V S G	
301	ACCAAGAAGGAGAACTGCCCCGTACAGCATCCTGGAGATAACATCAGTAGAAATCGGAGTT	360
	-----+-----+-----+-----+-----+-----+-----+	
	TGGTTCTTCCTCTTGACGGGCATGTCGTAGGACCTCTATTGTAGTCATCTTTAGCCTCAA	
	T K K E N C P Y S I L E I T S V E I G V	
361	GTTGCCGTCAAAGCCATTAACAGCAACTATTACTTAGCCATGAACAAGAAGGGGAAACTC	420
	-----+-----+-----+-----+-----+-----+-----+	
	CAACGGCAGTTTCGGTAATTGTCGTTGATAATGAATCGGTACTTGTTCTTCCCCTTTGAG	
	V A V K A I N S N Y Y L A M N K K G K L	
421	TATGGCTCAAAAGAATTTAACAATGACTGTAAGCTGAAGGAGAGGATAGAGGAAAATGGA	480
	-----+-----+-----+-----+-----+-----+-----+	
	ATACCGAGTTTTCTTAAATTGTTACTGACATTCGACTTCCTCTCCTATCTCCTTTTACCT	
	Y G S K E F N N D C K L K E R I E E N G	

MATCH WITH FIG. 1C

FIG.1B

MATCH WITH FIG. 1B

```

481  TACAATACCTATGCATCATTTAACTGGCAGCATAATGGGAGGCAAATGTATGTGGCATTG
-----+-----+-----+-----+-----+-----+-----+
ATGTTATGGATACGTAGTAAATTGACCGTCGTATTACCCTCCGTTTACATACACCGTAAC
      Y N T Y A S F N W Q H N G R Q M Y V A L
541  AATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAACACGAAGGAAAAACACCTCTGCTCAC
-----+-----+-----+-----+-----+-----+
TTACCTTTTCCTCGAGGTTCTCTCCTGTCTTTTGTGCTTCCTTTTGTGGAGACGAGTG
      N G K G A P R R G Q K T R R K N T S A H
601  TTTCTTCCAATGGTGGTACACTCATAG
-----+-----+-----+-----+-----+
AAAGAAGGTTACCACCATGTGAGTATC
      F L P M V V H S *

```

FIG.1C

	1					50
FGF4	MS.GPGTAAV	ALLPAVLLAL	LA.....	.PWAGRGGAA	APTAPNGTLE	
FGF6	MSRGAGRLQG	TLWALVFLGI	LV.....	.GMVVPSPAG	TR.ANNTLLD	
FGF5MSL	SFLLLLFFSH	LILSAWAHGE	KRLAPKGQPG	PAATDRNPIG	
FGF1	
FGF2	
FGF9MAPLGEVG	NYFGVQDAVP	
FGF7MHKW	ILTWILPTLLYRSCF	HIICLVGTIS	
KGF2MWKW	ILTHCASAFA	HLPGCCCCCF	LLLFLVSSVP	
FGF3MGL	IWLLLLSLLE	
FGF8	MGSPRSALSC	LLHLVLCL	QAQVRSAAQK	RGPGAGNPAD	TLGQGHEDRP	

	51					100
FGF4	AELERRWESL	VALSLARLPV	AA..QPKEAA	VQSGAGDY..	...LLGIKRL	
FGF6	S...RGWGTL	LSRSRAGLAG	EI.....AG	VNWESG.Y..	...LVGIKRQ	
FGF5	SSSRQSSSSA	MSSSSASSSP	AASLGSQGS	LEQSSFQW..	...SPSGRRT	
FGF1MAEG	EITTFTALTE	KFN...LPPGN..	...YK...KP	
FGF2MAAG	SITTLPALPE	DGGSGAFPPGH..	...FK...DP	
FGF9	FGNVPVLPVD	SPVLLSDHLG	QSEAGGLPRG	PAVTDLDH..	...LKGILRR	
FGF7	LACNDMTPEQ	M...ATNVNCSSPE	RHTRSYDY..	...MEGGDIR	
KGF2	VTCQALGQDM	VSPEATNSSS	SSFSSPSSAG	RHVRSYNH..	...LQ.GDVR	
FGF3	PGWPAAGPGARLRRDAG	GRGGVYEH..	...L.GGAPR	
FGF8	FGQRSRAGKN	FTNPAPNYPE	EGSKEQRDSV	LPKVTQRHVR	EQSLVTDQLS	

MATCH WITH FIG. 2B

FIG. 2A

MATCH WITH FIG. 2A

	101		150
FGF4	RRL.....YC NVGIGFHLQA	LPDGRIGGAH	ADT.RDSLLE LSPVERGV.V
FGF6	RRL.....YC NVGIGFHLQV	LPDGRISGTH	EEN.PYSLLE ISTVERGV.V
FGF5	GSL.....YC RVGIGFHLQI	YPDGKVNGSH	EAN.MLSVLE IFAVSQGI.V
FGF1	KLL.....YC SNG.GHFLRI	LPDGTVDGTR	DRSDQHIQLQ LSAESVGE.V
FGF2	KRL.....YC KNG.GFFLRI	HPDGRVDGVR	EKSDPHIKLQ LQAEERGV.V
FGF9	RQL.....YC R.T.GFHLEI	FPNGTIQGTR	KDHSRFGILE FISIAVGL.V
FGF7	VRR.....LF CRT.QWYLRI	DKRGKVKGTQ	EMKNNYNIME IRTVAVGI.V
KGF2	WRK.....LF SFT.KYFLKI	EKNGKVSQTK	KENCPYSILE ITSVEIGV.V
FGF3	RRK.....LY CAT.KYHLQL	HPSGRVNGSL	.ENSAYSILE ITAVEVGI.V
FGF8	RRLIRTYQLY	SRTSGKHVQV LANKRINAMA	EDGDPFAKLI VETDTFGSRV

	151		200
FGF4	SIFGVASRFF	VAMSSK GKLY	G.SPFFTDEC TFKEILLPNN YNAYESYKYP
FGF6	SLFGVRSALF	VAMNSKGRLY	A.TPSFQEEC KFRETLLPNN YNAYESDLYQ
FGF5	GIRGVFSNKF	LAMSKK GKLY	A.SAKFTDDC KFRERFQENS YNTYASAIHR
FGF1	YIKSTETGQY	LAMDTDGLLY	G.SQTPNEEC LFLERLEENH YNTYISKKH.
FGF2	SIKGVCANRY	LAMKEDGRLL	A.SKCVTDEC FFFERLESNN YNTYRSRKY.
FGF9	SIRGVDSGLY	LGMNEKGELY	G.SEKLTQEC VFREQFEENW YNTYSSONLYK
FGF7	AIKGVSESEFY	LAMNKEGKLY	A.KKECNEDC NFKELILENH YNTYAS....
KGF2	AVKAINSNNY	LAMNKK GKLY	G.SKEFNNDK KLKERIEENG YNTYAS....
FGF3	AIRGLFSGRY	LAMNKRGRLY	A.SEHYSAEC EFVERIHELG YNTYASRLYR
FGF8	RVRGAETGLY	ICMNKK GKLY	AKSNGK GKDC VFTEIVLENN YTALQNAKY.

MATCH WITH FIG. 2C

FIG.2B

MATCH WITH FIG. 2B

	201		250
FGF4 GM..... FI	ALSKNGKTKK G..NRVSPTM	KVTHFLPRL.
FGF6 GT..... YI	ALSKYGRVKR G..SKVSPIM	TVTHFLPRI.
FGF5 TEKTGREWYV	ALNKRKGAKR GCSPRVKPQH	ISTHFLPRFK
FGF1AEKNWFV	GLKKNGSCKR G..PRTHYGQ	KAILFLPLPV
FGF2T..SWYV	ALKRTGQYKL G..SKTGPGQ	KAILFLPMSA
FGF9	HV..... ..DTGRRYYV	ALNKDGTPRE G..TRTKRHQ	KFTHFLPRPV
FGF7AKW THNGGEM.FV	ALNQKGIPVR G..KKTKKEQ	KTAHFLPMAI
KGF2FNW QHNGRQM.YV	ALNGKGAPRR G..QKTRRKN	TSAHFLPMVV
FGF3	TVSSTPGARR QPSAERLWYV	SVNGKGRPRR G..FKTRRTQ	KSSLFLPRVL
FGF8EGWYM	AFTRKGRPRK G..SKTRQHQ	REVHFMKRLP

	251		300
FGF4
FGF6
FGF5	QSEQPELSFT VTVPEKKNPP	SPIKSKIPLS APRKNTNSVK	YRLKFRFG..
FGF1	SSD.....
FGF2	KS.....
FGF9	DPDKVPELYK DILSQS....
FGF7	T.....
KGF2	HS.....
FGF3	DHRDHEMVRQ LQSGLP RPPG	KGVP RRRRQ KQSPDNLEPS	HVQASRLGSQ
FGF8	RGHHTTEQSL RFEFLNYPPF	TRSLRGSQRT WAPEPR....

MATCH WITH FIG. 2D

FIG. 2C

MATCH WITH FIG. 2C

	301
FGF4
FGF6
FGF5
FGF1
FGF2
FGF9
FGF7
<i>KGF2</i>
FGF3	LEASAH
FGF8

FIG.2D

GGAATTCCGG GAAGAGAGGG AAGAAAACAA CGGCGACTGG GCAGCTGCCT CCACTTCTGA	60
CAACTCCAAA GGGATATACT TGTAGAAGTG GCTCGCAGGC TGGGGCTCCG CAGAGAGAGA	120
CCAGAAGGTG CCAACCGCAG AGGGGTGCAG ATATCTCCCC CTATTCCCCA CCCCACCTCC	180
CTTGGGTTTT GTTCACCGTG CTGTCATCTG TTTTTCAGAC CTTTTTGGCA TCTAACATGG	240
TGAAGAAAGG AGTAAAGAAG AGAACAAAGT AACTCCTGGG GGAGCGAAGA GCGCTGGTGA	300
CCAACACCAC CAACGCCACC ACCAGCTCCT GCTGCTGCGG CCACCCACGT CCACCATTTA	360
CCGGGAGGCT CCAGAGGCGT AGGCAGCGGA TCCGAGAAAG GAGCGAGGGG AGTCAGCCGG	420
CTTTTCCGAG GAGTTATGGA TGTTGGTGCA TTCACTTCTG GCCAGATCCG CGCCCAGAGG	480
GAGCTAACCA GCAGCCACCA CCTCGAGCTC TCTCCTTGCC TTGCATCGGG TCTTACCCTT	540
CCAGTATGTT CTTTCTGATG AGACAATTC CAGTGCCGAG AGTTTCAGTA CA ATG Met	595
TGG AAA TGG ATA CTG ACA CAT TGT GCC TCA GCC TTT CCC CAC CTG CCC Trp Lys Trp Ile Leu Thr His Cys Ala Ser Ala Phe Pro His Leu Pro	643
GGC TGC TGC TGC TGC TGC TTT TTG TTG CTG TTC TTG GTG TCT TCC GTC Gly Cys Cys Cys Cys Cys Phe Leu Leu Leu Phe Leu Val Ser Ser Val	691
CCT GTC ACC TGC CAA GCC CTT GGT CAG GAC ATG GTG TCA CCA GAG GCC Pro Val Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu Ala	739
ACC AAC TCT TCT TCC TCC TCC TTC TCC TCT CCT TCC AGC GCG GGA AGG Thr Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly Arg	787
CAT GTG CGG AGC TAC AAT CAC CTT CAA GGA GAT GTC CGC TGG AGA AAG His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys	835
CTA TTC TCT TTC ACC AAG TAC TTT CTC AAG ATT GAG AAG AAC GGG AAG Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys	883
GTC AGC GGG ACC AAG AAG GAG AAC TGC CCG TAC AGC ATC CTG GAG ATA Val Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile	931
ACA TCA GTA GAA ATC GGA GTT GTT GCC GTC AAA GCC ATT AAC AGC AAC Thr Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn	979
TAT TAC TTA GCC ATG AAC AAG AAG GGG AAA CTC TAT GGC TCA AAA GAA Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu	1027
TTT AAC AAT GAC TGT AAG CTG AAG GAG AGG ATA GAG GAA AAT GGA TAC Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr	1075

FIG.3A

AAT ACC TAT GCA TCA TTT AAC TGG CAG CAT AAT GGG AGG CAA ATG TAT Asn Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr	1123
GTG GCA TTG AAT GGA AAA GGA GCT CCA AGG AGA GGA CAG AAA ACA CGA Val Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg	1171
AGG AAA AAC ACC TCT GCT CAC TTT CTT CCA ATG GTG GTA CAC TCA Arg Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser	1216
TAGAGGAAGG CAACGTTTGT GGATGCAGTA AAACCAATGG CTCTTTTGCC AAGAATAGTG	1276
GATATTCTTC ATGAAGACAG TAGATTGAAA GGCAAAGACA CGTTGCAGAT GTCTGCTTGC	1336
TTAAAAGAAA GCCAGCCTTT GAAGGTTTTT GTATTCAGTG CTGACATATG ATGTTCTTTT	1396
AATTAGTTCT GTGTCATGTC TTATAATCAA GATATAGGCA GATCGAATGG GATAGAAGTT	1456
ATTCCCAAGT GAAAAACATT GTGGCTGGGT TTTTGTGTTG TGTTGTCAAG TTTTGTGTTT	1516
TAAACCTCTG AGATAGAACT TAAAGGACAT AGAACAATCT GTTGAAAGAA CGATCTTCGG	1576
GAAAGTTATT TATGGAATAC GAACTCATAT CAAAGACTTC ATTGCTCATT CAAGCCTAAT	1636
GAATCAATGA ACAGTAATAC GTGCAAGCAT TTAAGGAAA GCACTTGGGT CATATCATAT	1696
GCACAACCAA AGGAGTTCTG GATGTGGTCT CATGGAATAA TTGAATAGAA TTTAAAAATA	1756
TAAACATGTT AGTGTGAAAC TGTTCTAACA ATACAAATAG TATGGTATGC TTGTGCATTC	1816
TGCCTTCATC CCTTTCTATT TCTTTCTAAG TTATTTATTT AATAGGATGT TAAATATCTT	1876
TTGGGGTTTT AAAGAGTATC TCAGCAGCTG TCTTCTGATT TATCTTTTCT TTTTATTCAG	1936
CACACCACAT GCATGTTTAC GACAAAGTGT TTTTAAACT TGGCGAACAC TTCAAAAATA	1996
GGAGTTGGGA TTAGGGAAGC AGTATGAGTG CCCGTGTGCT ATCAGTTGAC TTAATTTGCA	2056
CTTCTGCAGT AATAACCATC AACAATAAAT ATGGCAATGC TGTGCCATGG CTTGAGTGAG	2116
AGATGTCTGC TATCATTTGA AAACATATAT TACTCTCGAG GCTTCCTGTC TCAAGAAATA	2176
GACCAGAAGG CCAAATTCTT CTCTTTCAAT ACATCAGTTT GCCTCCAAGA ATATACTAAA	2236
AAAAGGAAAA TTAATTGCTA AATACATTTA AATAGCCTAG CCTCATTATT TACTCATGAT	2296
TTCTTGCCAA ATGTCATGGC GGTAAAGAGG CTGTCCACAT CTCTAAAAAC CCTCTGTAAA	2356
TTCCACATAA TGCATCTTTC CCAAAGGAAC TATAAAGAAT TTGGTATGAA GCGCAACTCT	2416

FIG.3B

CCCAGGGGCT	TAAACTGAGC	AAATCAAATA	TATACTGGTA	TATGTGTAAC	CATATACAAA	2476
AACCTGTTCT	AGCTGTATGA	TCTAGTCTTT	ACAAAACCAA	ATAAACTTG	TTTTCTGTAA	2536
ATTTAAAGAG	CTTTACAAGG	TTCCATAATG	TAACCATATC	AAAATTCATT	TTGTTAGAGC	2596
ACGTATAGAA	AAGAGTACAT	AAGAGTTTAC	CAATCATCAT	CACATTGTAT	TCCACTAAAT	2656
AAATACATAA	GCCTTATTTG	CAGTGTCTGT	AGTGATTTTA	AAAATGTAGA	AAAATACTAT	2716
TTGTTCTAAA	TACTTTTAAG	CAATAACTAT	AATAGTATAT	TGATGCTGCA	GTTTTATCTT	2776
CATATTTCTT	GTTTTGAAAA	AGCATTTTAT	TGTTTGGACA	CAGTATTTTG	GTACAAAAAA	2836
AAAGACTCAC	TAAATGTGTC	TTACTAAAGT	TTAACCTTTG	GAAATGCTGG	CGTTCTGTGA	2896
TTCTCCAACA	AAC TTATTTG	TGTCAATACT	TAACCAGCAC	TTCCAGTTAA	TCTGTTATTT	2956
TTAAAAATTG	CTTTATTAAG	AAATTTTTTG	TATAATCCCA	TAAAAGGTCA	TATTTTTCCC	3016
ATTCTTCAAA	AAA ACTGTAT	TTCAGAAGAA	ACACATTTGA	GGCACTGTCT	TTGGCTTAT	3076
AGTTTAAATT	GCATTT CATC	ATACTTTGCT	TCCA ACTTGC	TTTTTG GCAA	ATGAGATTAT	3136
AAAAATGTTT	AATTTTTGTG	GTTGGAATCT	GGATGTTAAA	ATTTAATTGG	TA ACTCAGTC	3196
TGTGAGCTAT	AATGTAATGC	ATTCCTATCC	AAACTAGGTA	TCTTTTTTTC	CTTTATGTTG	3256
AAATAATAAT	GGCACCTGAC	ACATAGACAT	AGACCACCCA	CAACCTAAAT	TAAATGTTTG	3316
GTAAGACAAA	TACACATTGG	ATGACCACAG	TAACAGCAAA	CAGGGCACAA	ACTGGATTCT	3376
TATTTACAT	AGACATTTAG	ATTACTAAAG	AGGGCTATGT	GTAAACAGTC	ATCATTATAG	3436
TACTCAAGAC	ACTAAAACAG	CTTCTAGCCA	AATATATTAA	AGCTTGCAGA	GGCCAAAAAT	3496
AGAAAACATC	TCCCCTGTCT	CTCCACATT	TCCCTCACAG	AAAGACAAAA	AACCTGCCTG	3556
GTGCAGTAGC	TCACACCTGT	AATCCCAGCA	GTTTGGGAGA	CTGTGGGAAG	ATGGCTTGAG	3616
TCCAGGAGTT	CTAGACAGGC	CTGAGAAACC	TAGTGAGACA	TCCTTCTCTT	AAACAAAACA	3676
AAACAAAACA	AATGTAGCCA	TGCGTGGTGG	CATATACCTG	TGGTCCCAAC	TACTCAGGAG	3736
GCTGAAACGG	AAGGATCTCT	TGGGCCCCAG	GAGTTTGAGG	CTGCAGTGAG	CTATAATCTT	3796
GCCATTGCAC	TCCAGCCTGG	GTGAAAAAGA	GCCAGAAAGA	AAGGAAAGAG	AGAAAAGAGA	3856
AAAGAAAGAG	AGAAAAGACA	GAAAGACAGG	AAGGAAGGAA	GGAAGGAAGG	AAGGAAGGAA	3916
GGAAGCAAGG	AAAGAAGGAA	GGAAGGAAAG	AAGGGAGGGA	AGGAAGGAGA	GAGAAAGAAA	3976
GATTGTTTGG	TAAGGAGTAA	TGACATTCTC	TTGCATTTAA	AAGTGGCATA	TTTGCTTGAA	4036

FIG.3C

ATGGAATAG AATTCTGGTC CCTTTTGCAA CTACTGAAGA AAAAAAAAAAG CAGTTTCAGC	4096
CCTGAATGTT GTAGATTGTA AAAAAAAAAA AAAAAAACTC GAGGGGGGGC CCGTACCCAA	4156
TTCGCCCTAT AGTGAGTCGT A	4177

FIG.3D

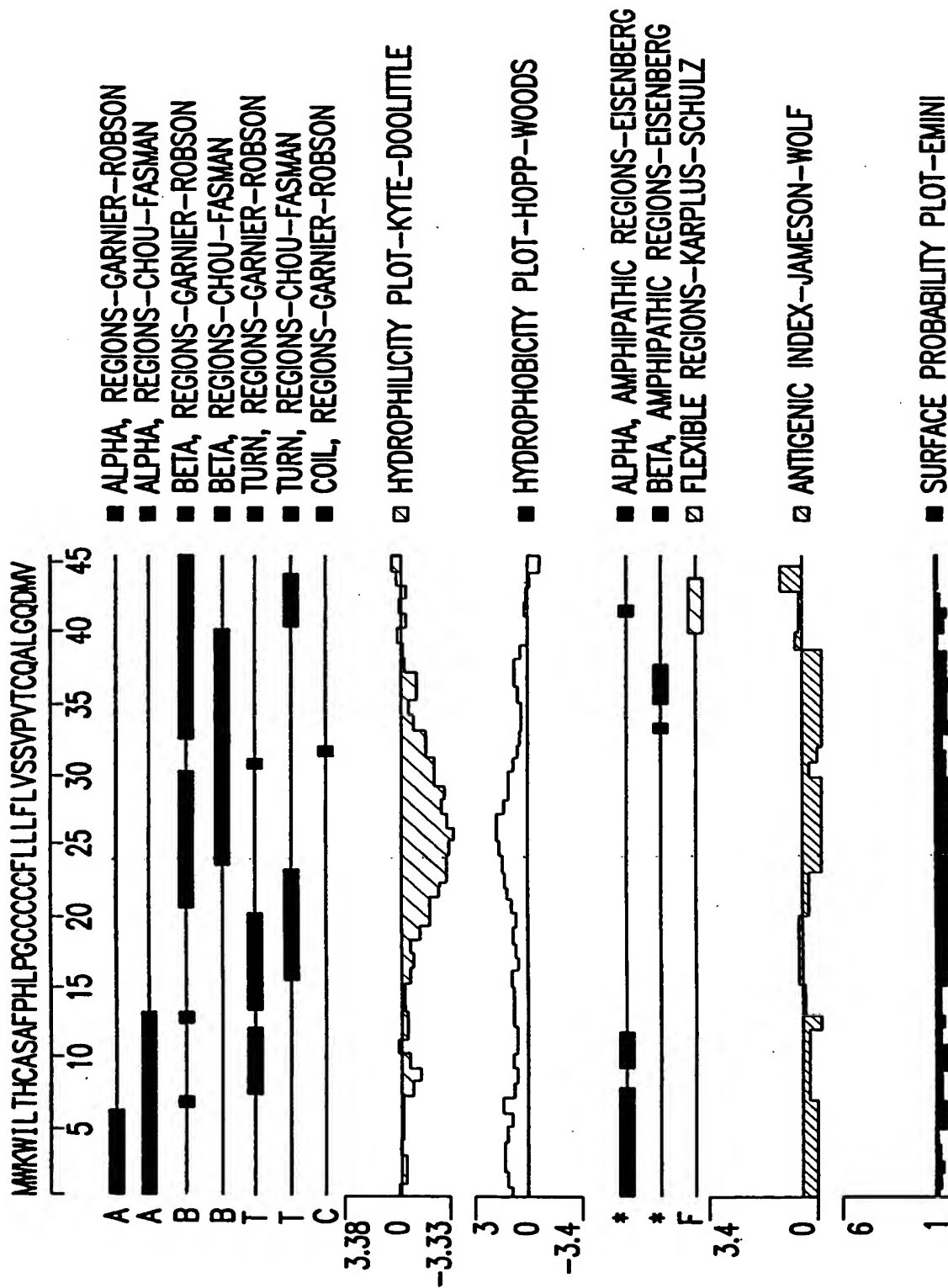
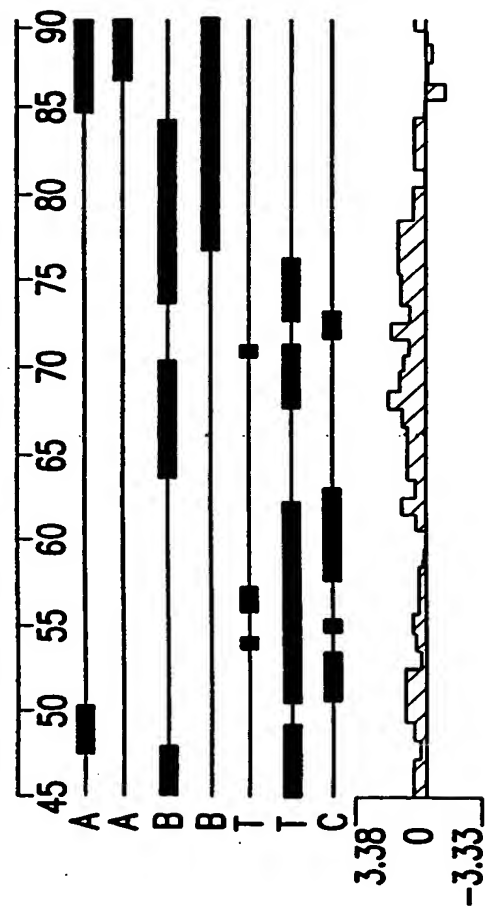
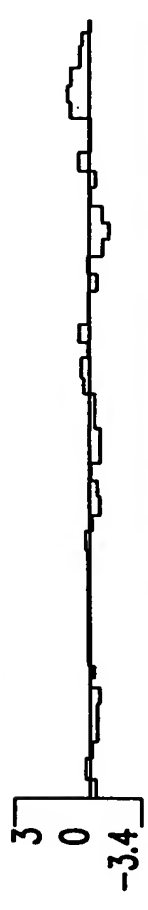


FIG.4A

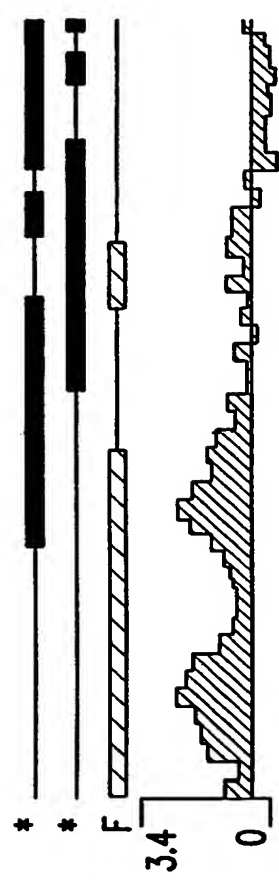
SPEATNSSSFSPPSAGRHVRSYNHLQGDVRMRKLFSTKYFL



- ALPHA, REGIONS-GARNIER-ROBSON
- ALPHA, REGIONS-CHOU-FASMAN
- BETA, REGIONS-GARNIER-ROBSON
- BETA, REGIONS-CHOU-FASMAN
- TURN, REGIONS-GARNIER-ROBSON
- TURN, REGIONS-CHOU-FASMAN
- COIL, REGIONS-GARNIER-ROBSON
- HYDROPHILICITY PLOT-KYTE-DOOLITTLE



- HYDROPHOBICITY PLOT-HOPP-WOODS



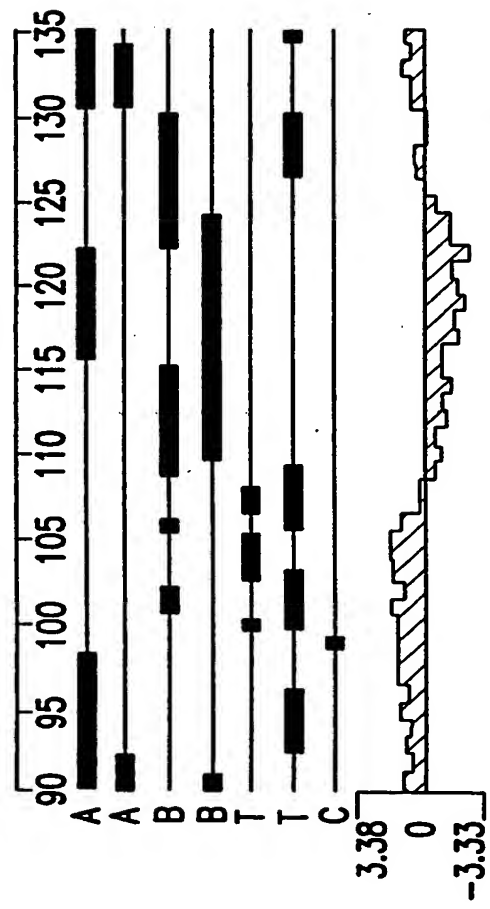
- ALPHA, AMPHIPATHIC REGIONS-EISENBERG
- BETA, AMPHIPATHIC REGIONS-EISENBERG
- FLEXIBLE REGIONS-KARPLUS-SCHULZ



- SURFACE PROBABILITY PLOT-EMINI

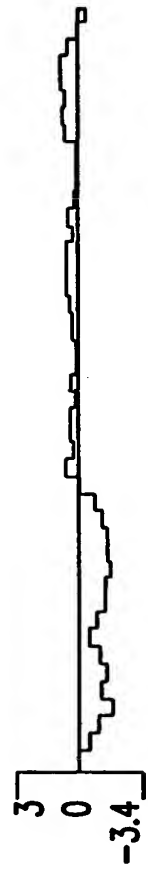
FIG.4B

KIEKNGKVSQTKKENCPSYLEITSVEIGWAWKAINSYYLAMN

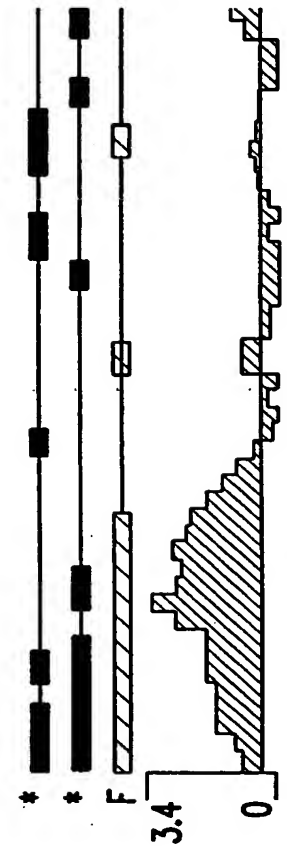


- ALPHA, REGIONS-GARNIER-ROBSON
- ALPHA, REGIONS-CHOU-FASMAN
- BETA, REGIONS-GARNIER-ROBSON
- BETA, REGIONS-CHOU-FASMAN
- TURN, REGIONS-GARNIER-ROBSON
- TURN, REGIONS-CHOU-FASMAN
- COIL, REGIONS-GARNIER-ROBSON

□ HYDROPHILICITY PLOT-KYTE-DOOLITTLE

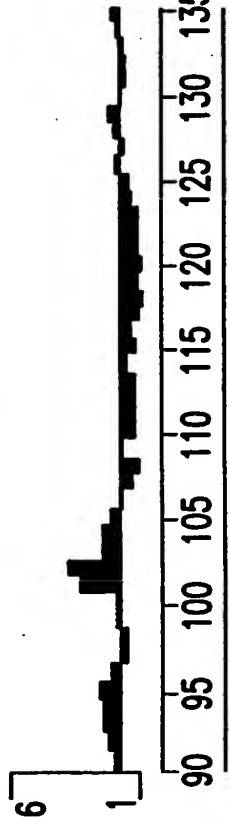


□ HYDROPHOBICITY PLOT-HOPP-WOODS



- ALPHA, AMPHIPATHIC REGIONS-EISENBERG
- BETA, AMPHIPATHIC REGIONS-EISENBERG
- FLEXIBLE REGIONS-KARPLUS-SCHULZ

□ ANTIGENIC INDEX-JAMESON-WOLF



■ SURFACE PROBABILITY PLOT-EMINI

FIG.4C

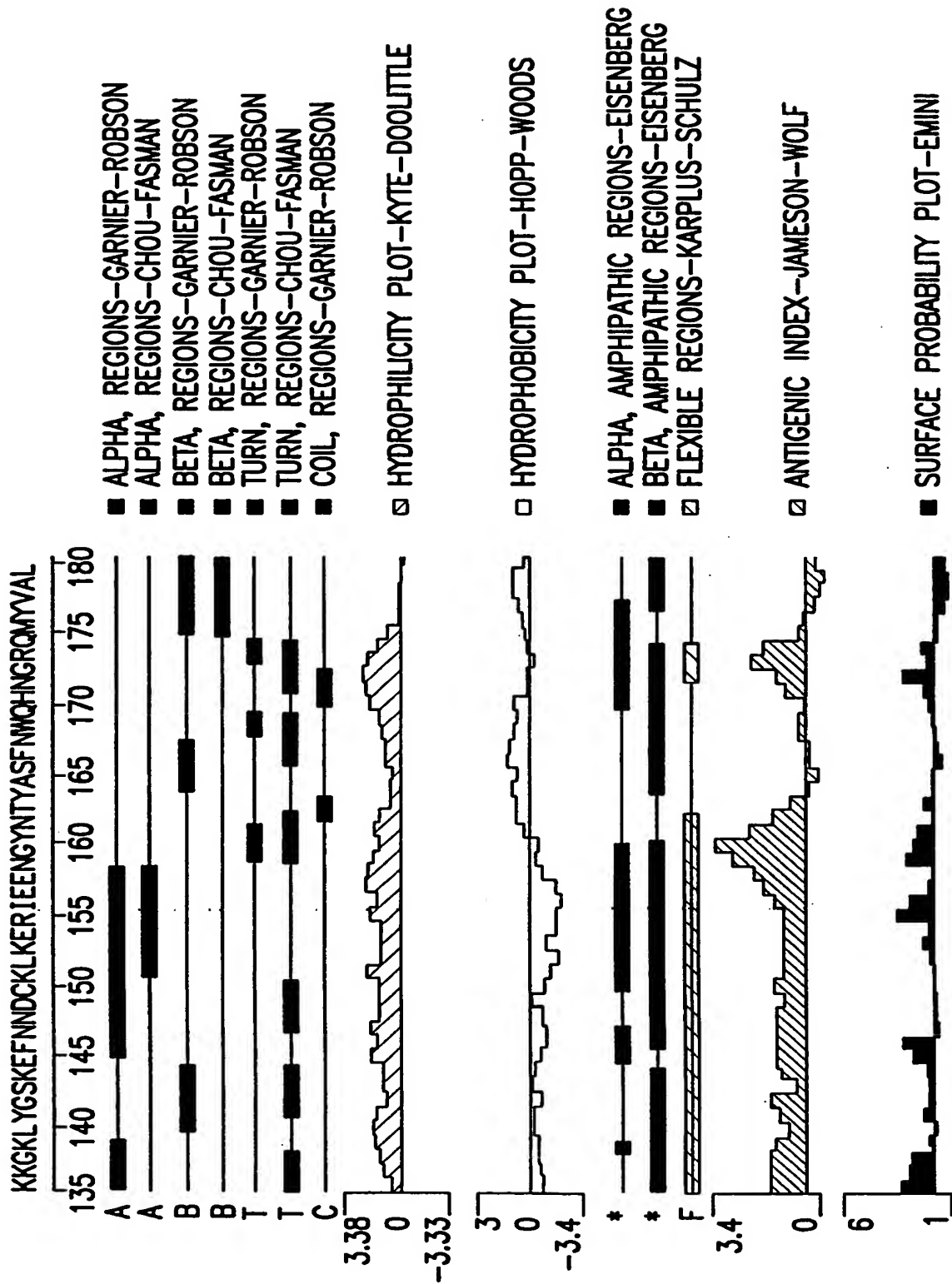


FIG.4D

NGKGAPRRGQKTRRKNTSAHFLPMVHVS

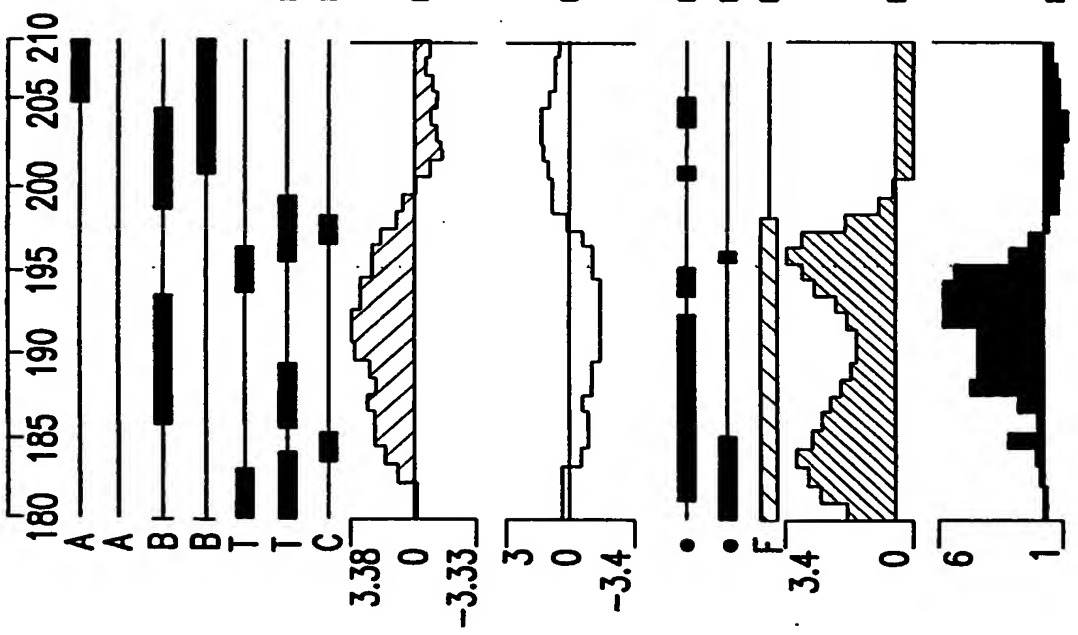


FIG.4E

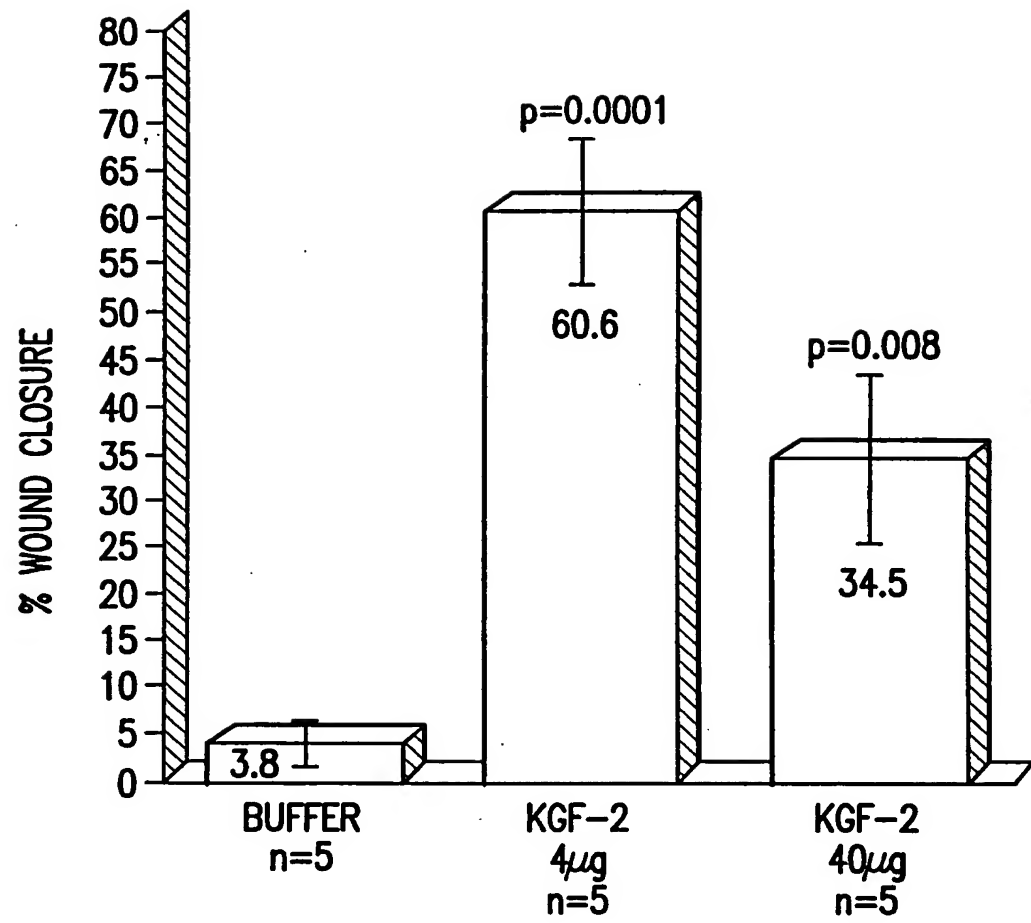


FIG.5

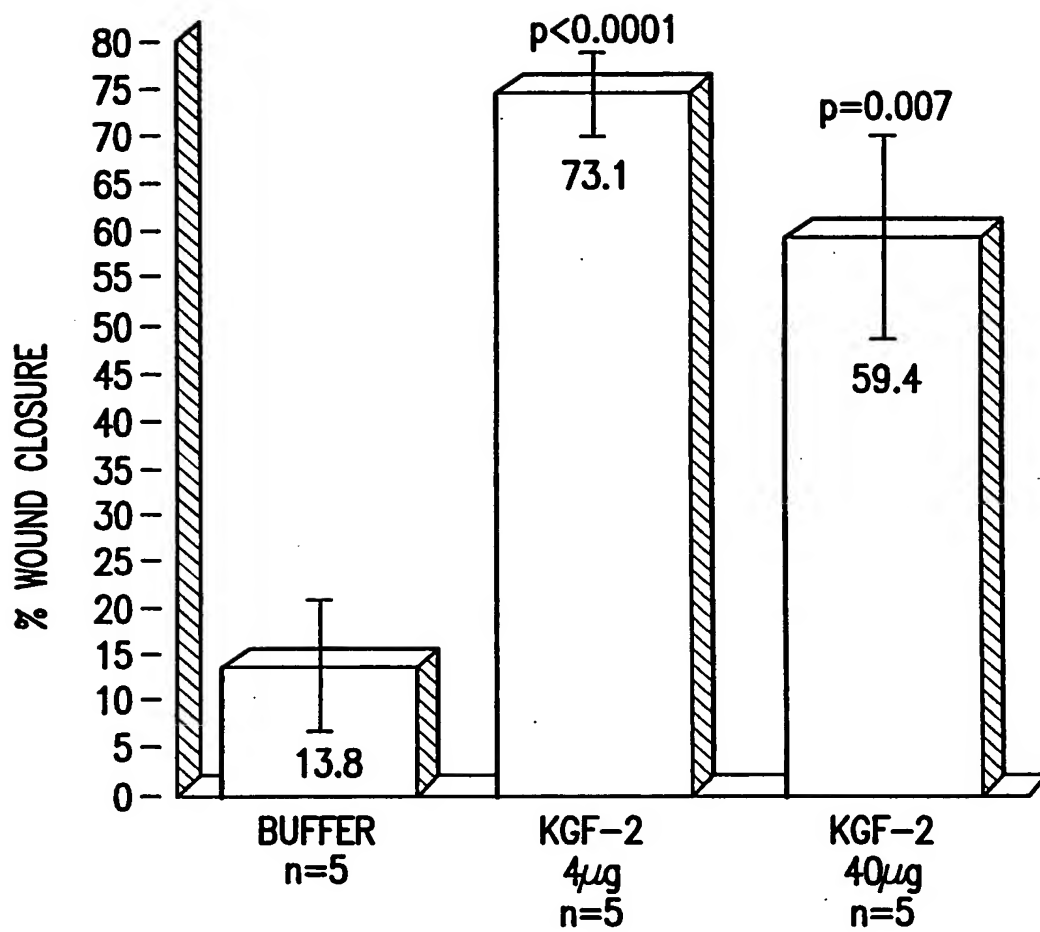


FIG.6

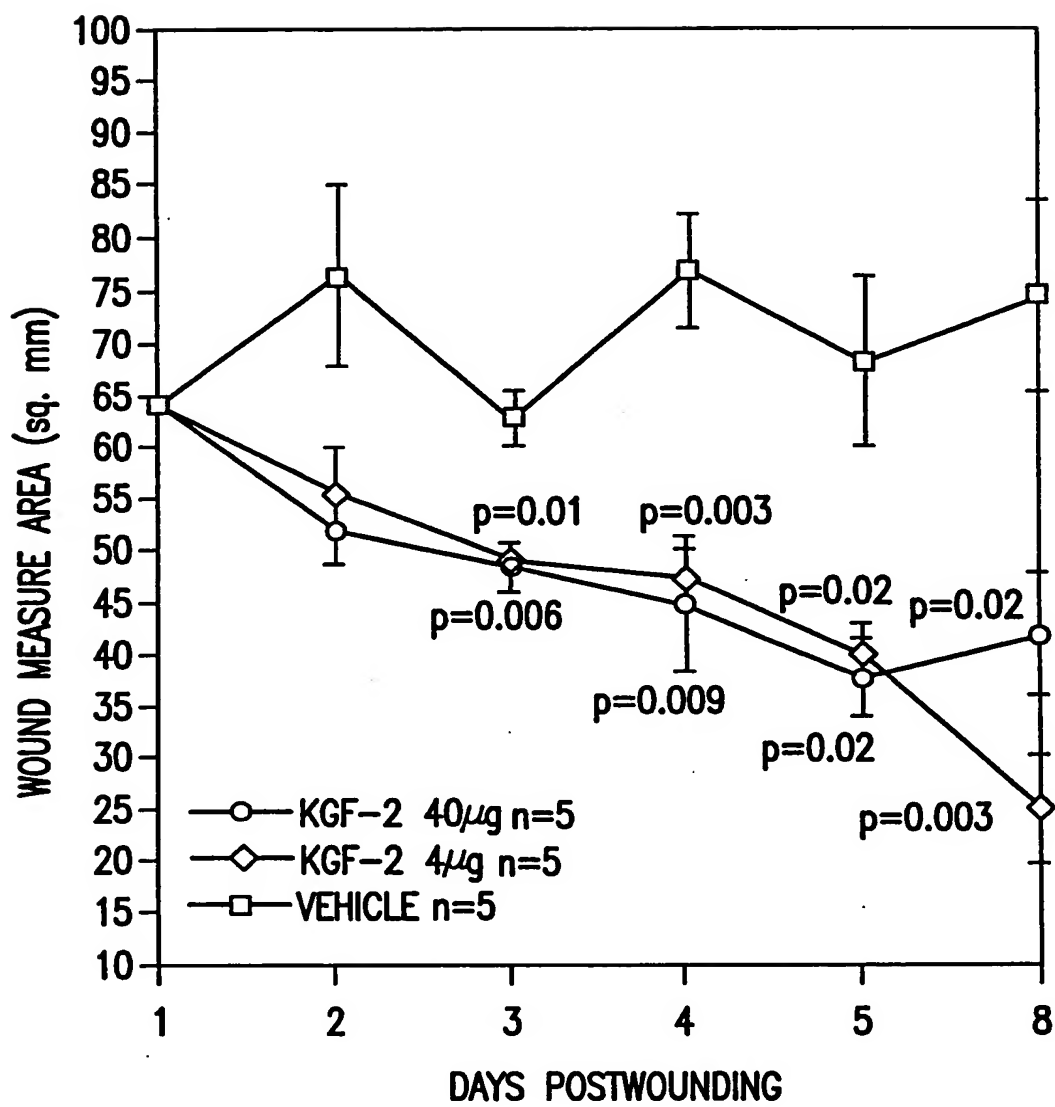


FIG.7

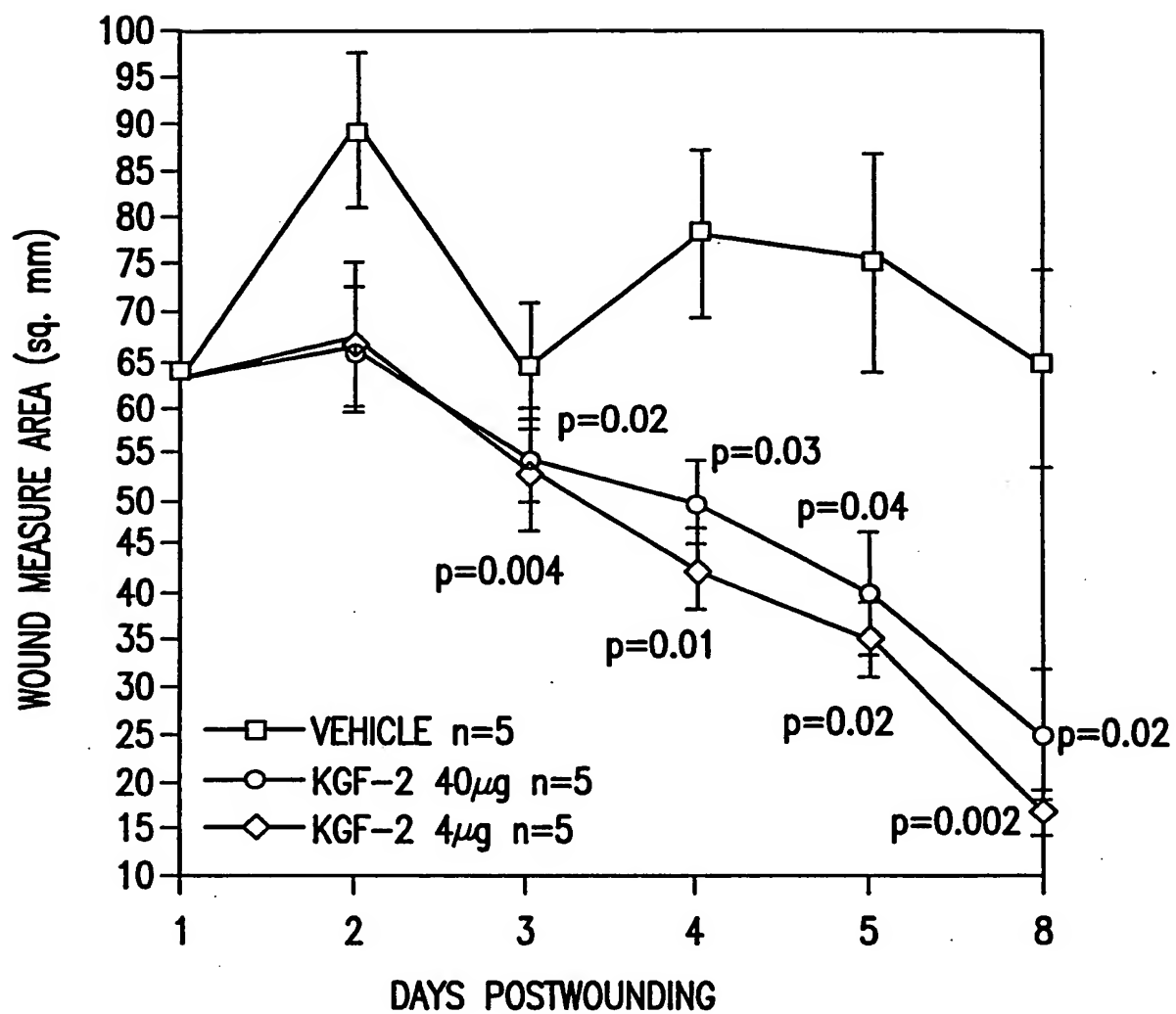
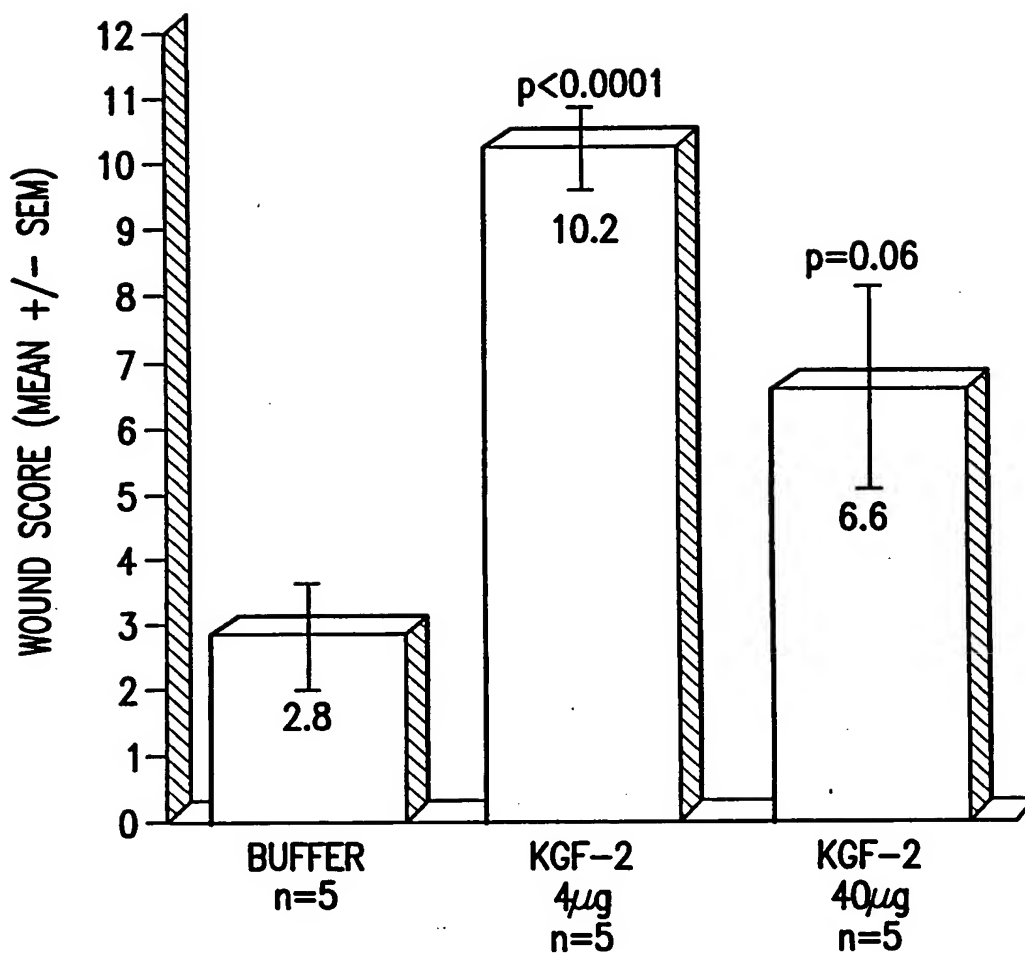
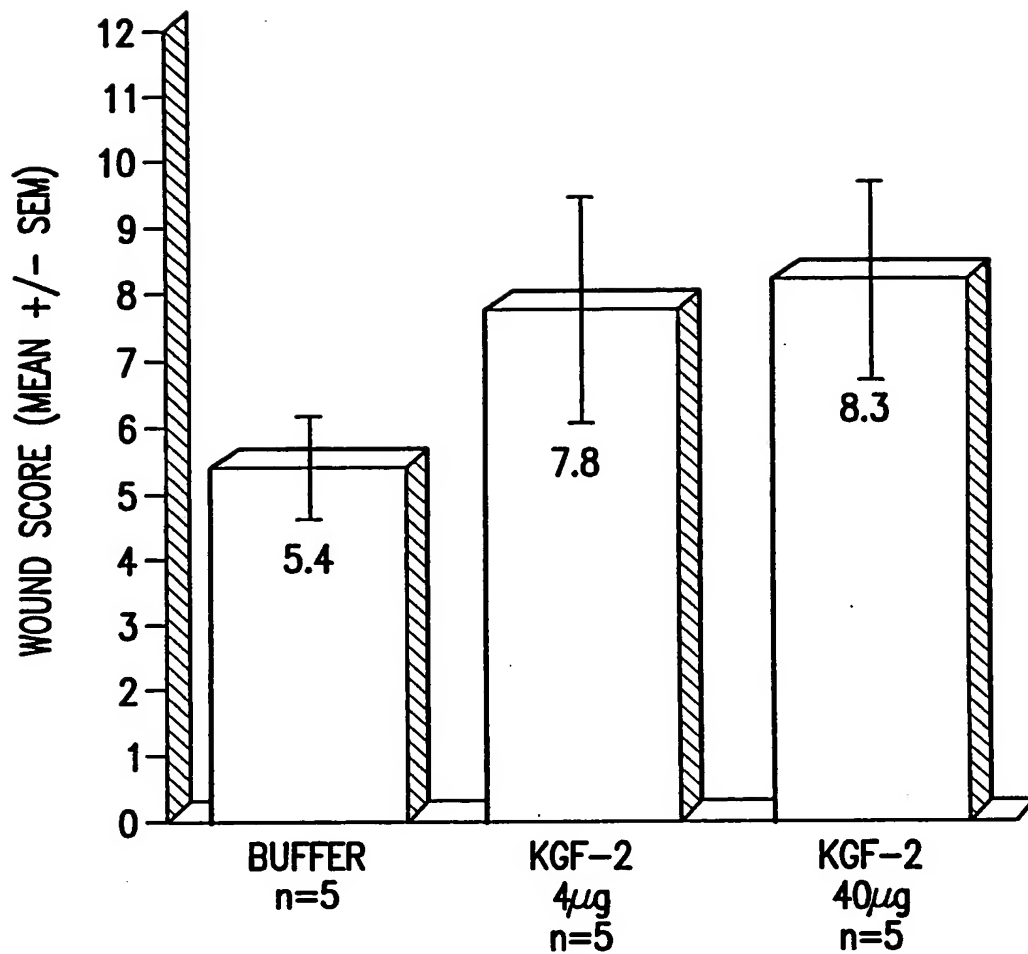


FIG.8



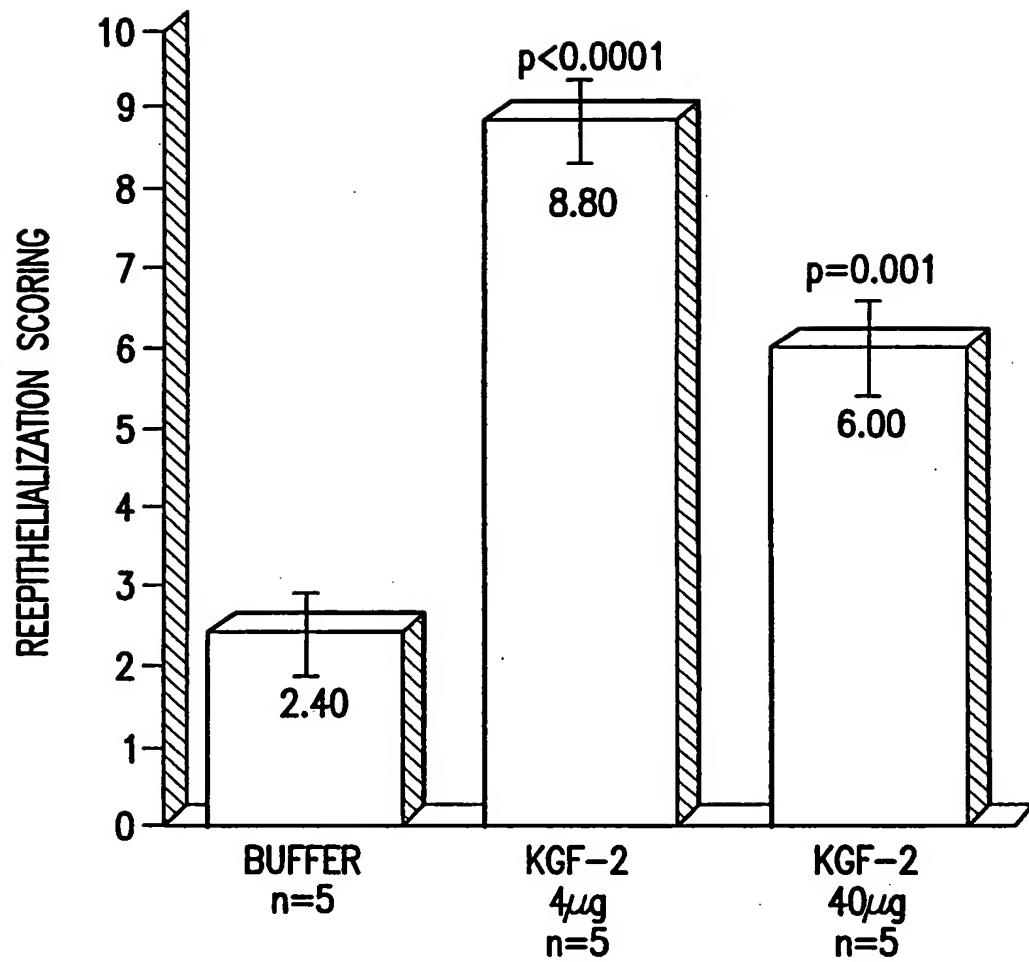
1-3 MINIMAL CELL ACCUMULATION, NO GRANULATION
4-6 IMMATURE GRANULATION, INFLAMMATORY CELLS, CAPILLARIES
10-12 FIBROBLASTS, COLLAGEN, EPITHELIUM

FIG.9



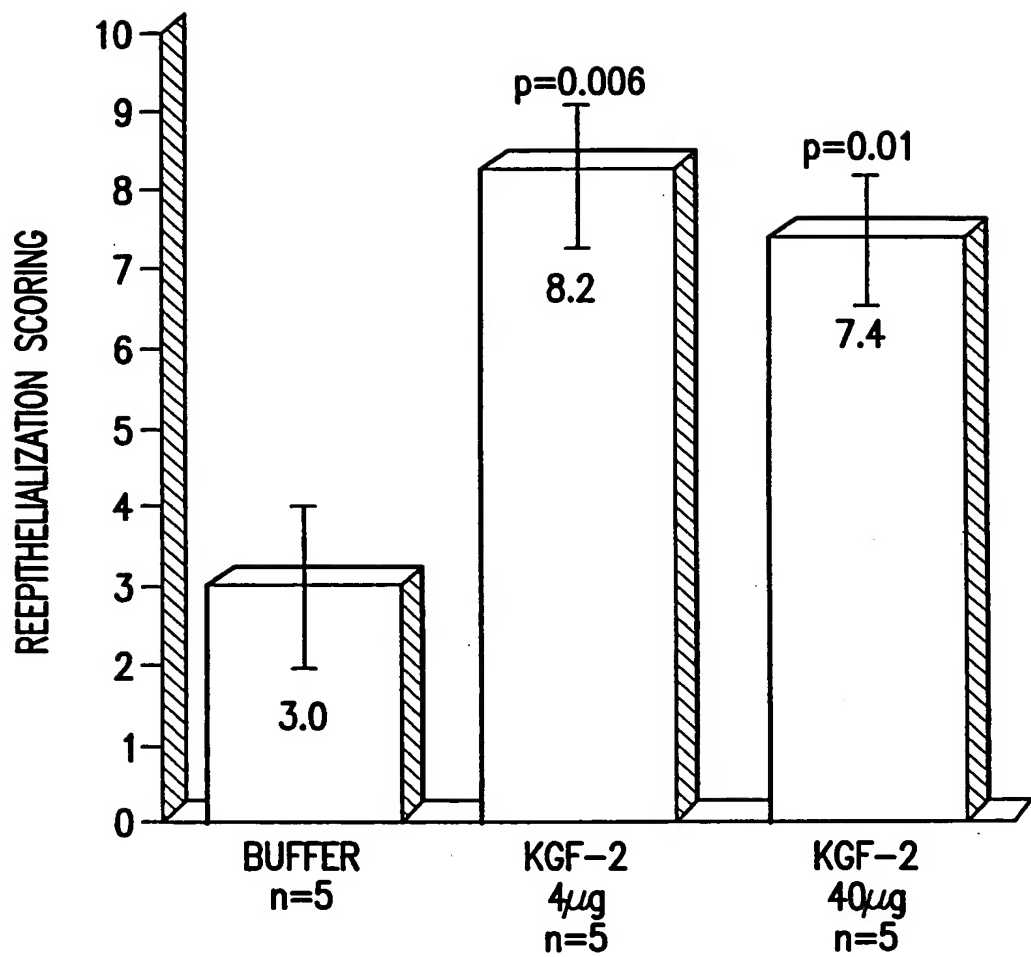
1-3 MINIMAL CELL ACCUMULATION, NO GRANULATION
4-6 IMMATURE GRANULATION, INFLAMMATORY CELLS, CAPILLARIES
7-9 GRANULATION TISSUE, CELLS, FIBROBLASTS, NEW EPITHELIUM
10-12 FIBROBLASTS, COLLAGEN, EPITHELIUM

FIG.10



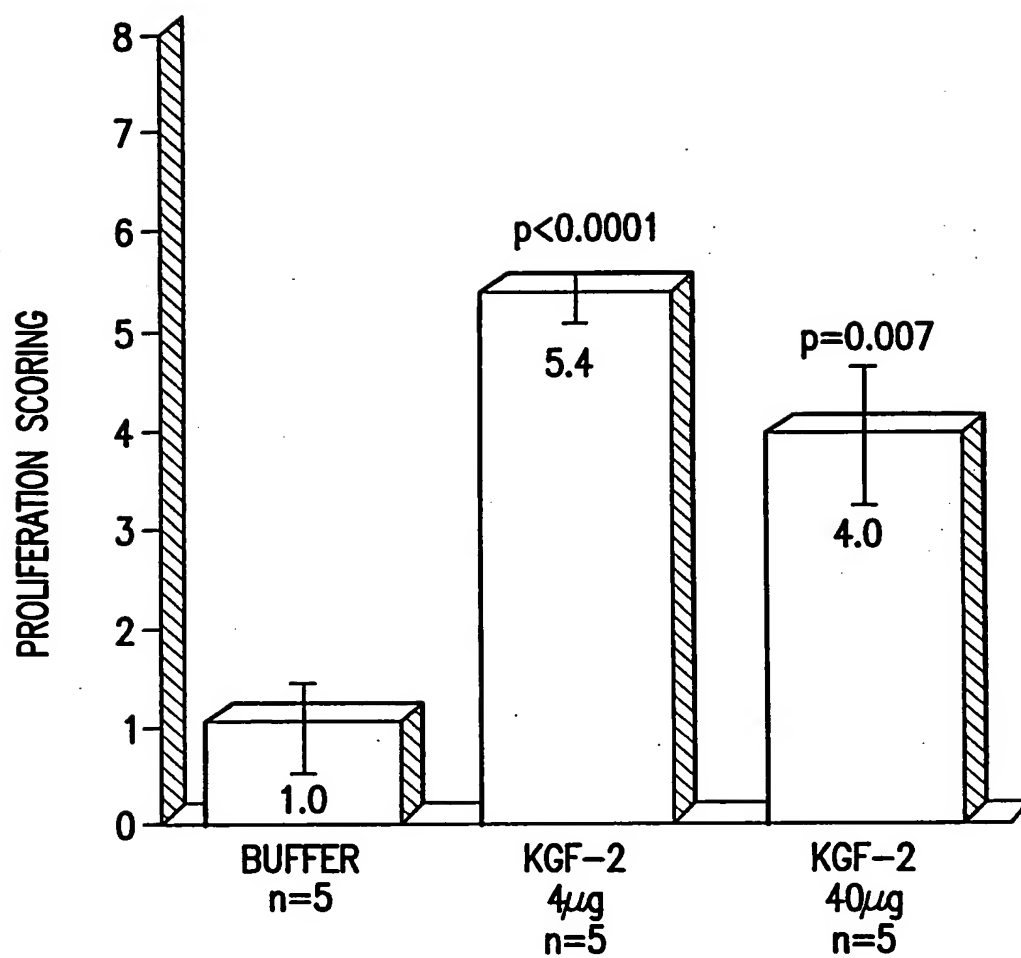
ANTI-CYTOKERATIN IMMUNOSTAINING
0-NO CLOSURE
5-SLIGHT TO MODERATE CLOSURE
10-COMPLETE CLOSURE

FIG.11



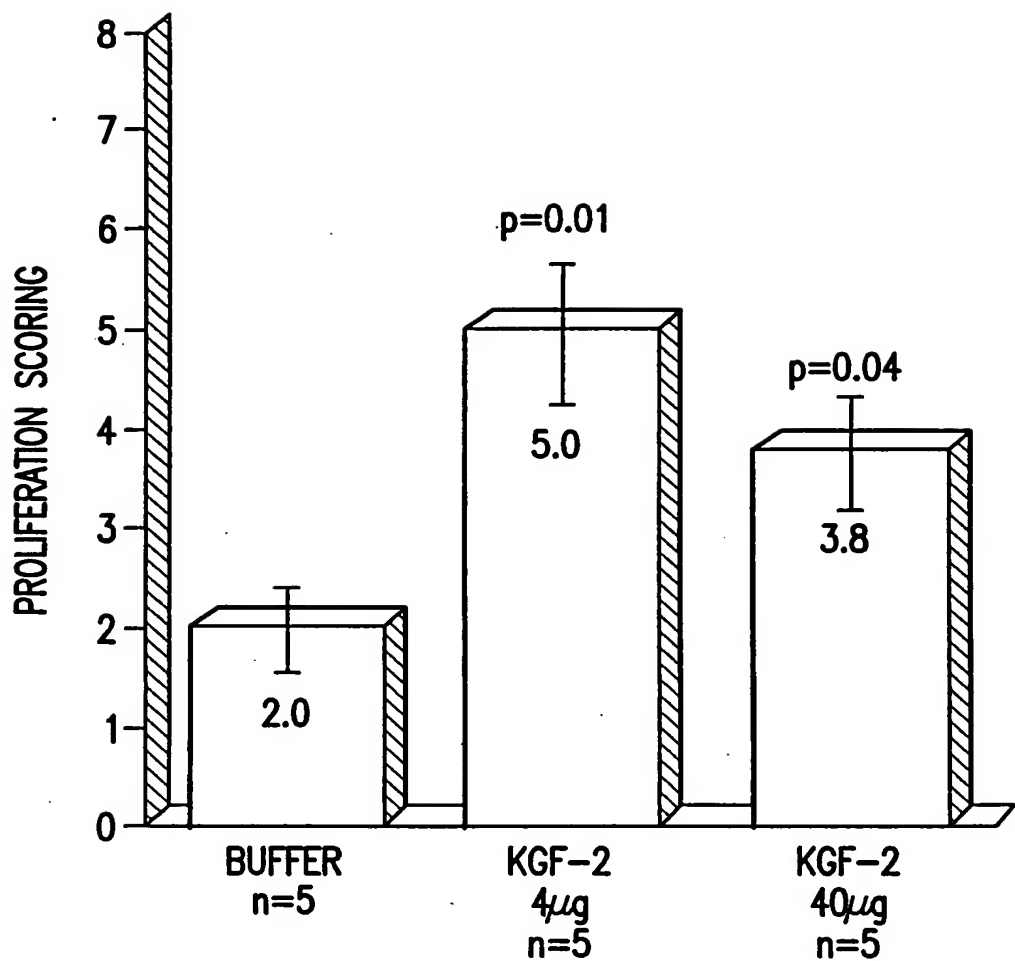
ANTI-CYTOKERATIN IMMUNOSTAINING
0-NO CLOSURE
5-SLIGHT TO MODERATE CLOSURE
10-COMPLETE CLOSURE

FIG.12



PCNA SCORING
0-2 SLIGHT PROLIFERATION
3-5 MODERATE PROLIFERATION
6-8 INTENSE PROLIFERATION

FIG.13



PCNA SCORING
0-2 SLIGHT PROLIFERATION
3-5 MODERATE PROLIFERATION
6-8 INTENSE PROLIFERATION

FIG.14

ATGAGAGGATCGCATCACCATCACCATCACGGATCCTGCCAGGCTCTGGGTC
AGGACATGGTTTCTCCGGAAGCTACCAACTCTTCTCTTCTTTCTTTCCC
CGTCTTCCGCTGGTCGTACGTTGTTCTTACAACCACCTGCAGGGTGACGTTT
GTTGGCGTAAACTGTTCTTTTACCAAATACTTCTGAAAATCGAAAAA
AACGGTAAAGTTTCTGGGACCAAGAAGGAGAACTGCCCGTACAGCATCCTG
GAGATAACATCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAACAG
CAACTATTACTTAGCCATGAACAAGAAGGGGAACTCTATGGCTCAAAG
AATTTAACAATGACTGTAAGCTGAAGGAGAGGATAGAGGAAAATGGAT
ACAATACCTATGCATCATTTAACTGGCAGCATAATGGGAGGCAAATGTAT
GTGGCATTGAaTGGAAAAGGAGCTCCAaGGAGAGGACAGAAAACACGAAG
GAAAAACACCTCTGCTCACTTTCTTCCAATGGTGGTACACTCATAG

MRGSHHHHHGSCQALGQDMVSPEATNSSSSSFSSPSSAGRHVRSYNHLQGD
VRWRKLFSTKYFLKIEKNGKVSGTKKENCYPYSILEITSVEIGVVAVKAINSN
YYLAMNKKGKLYGSKEFNNDCKLKERIEENGYNTYASFNWQHNGRQMYVA
LNGKGAPRRGQKTRRKNTSAHFLPMVVHS

kgf-2 synthetic cys37 Bam HI
AAAGGATCCTGCCAGGCTCTGGGTCAGGACATG

FIG.15

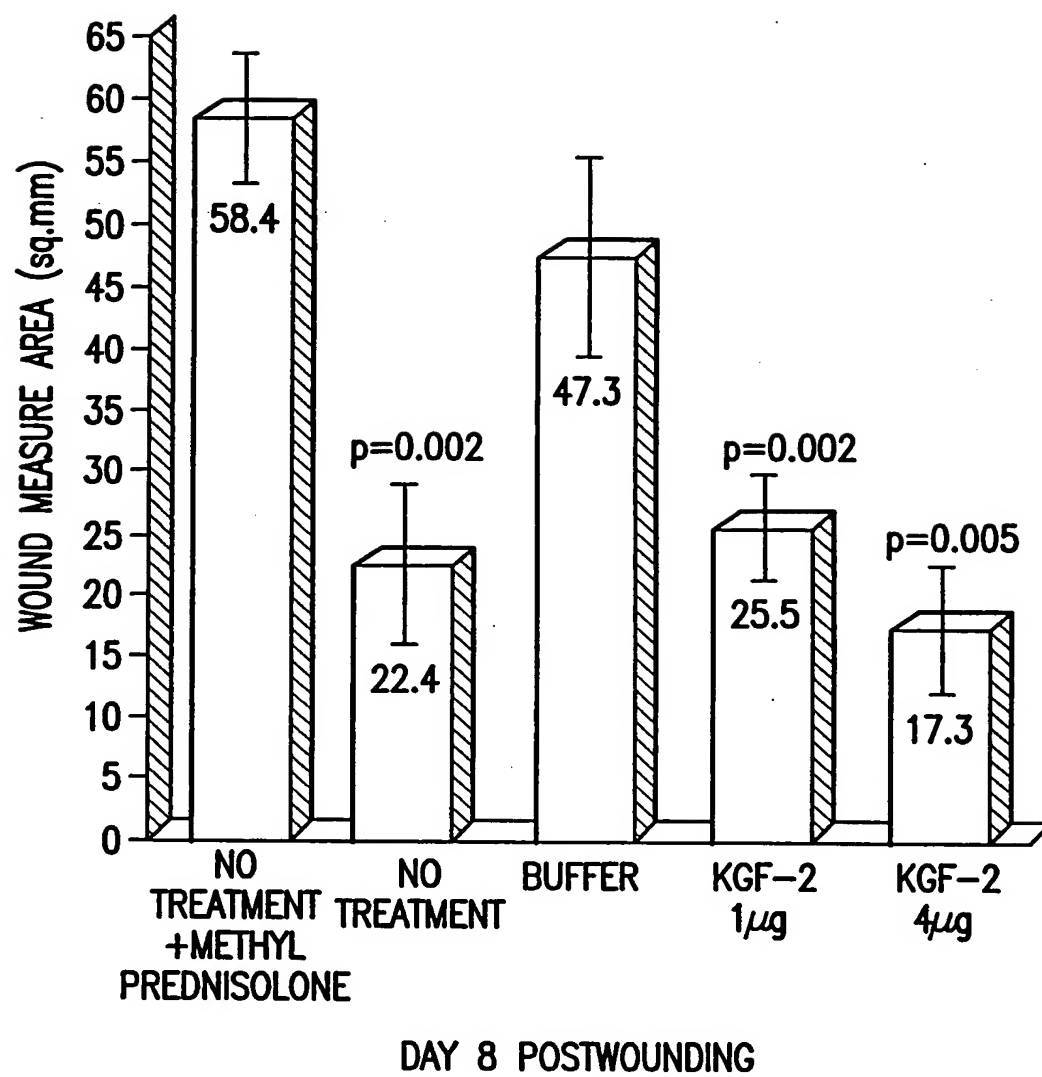
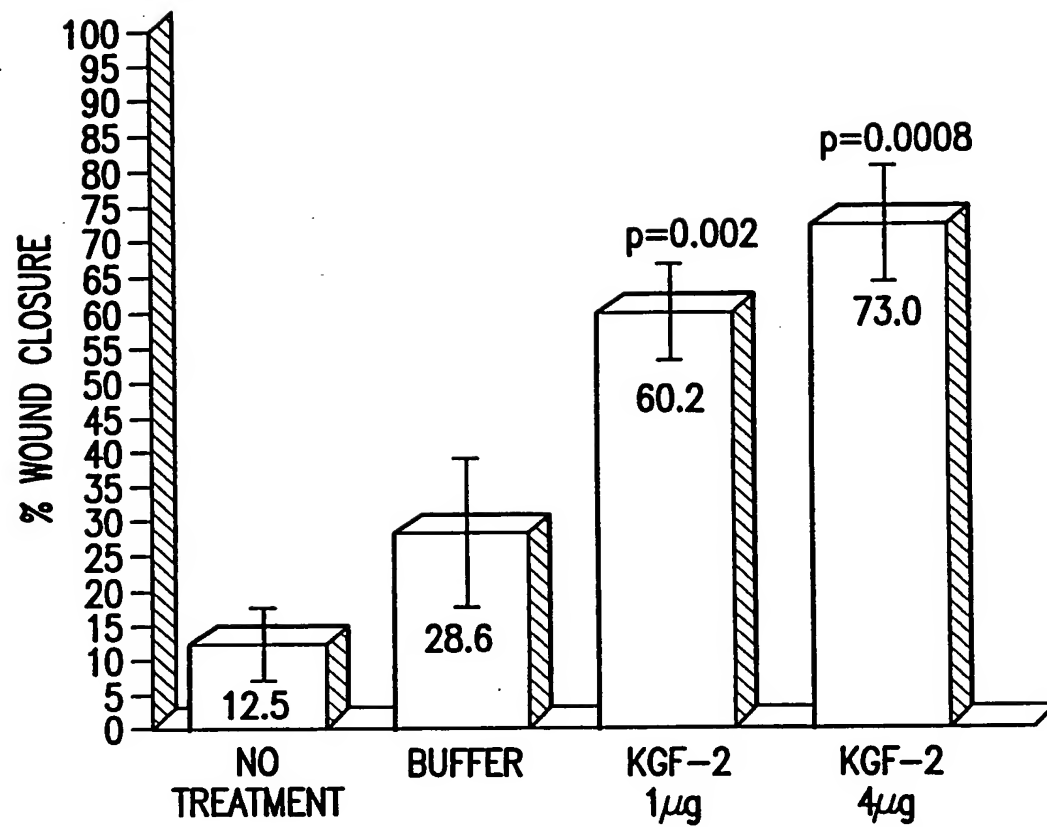


FIG.16



GLUCOCORTICOID TREATED ANIMALS

FIG.17

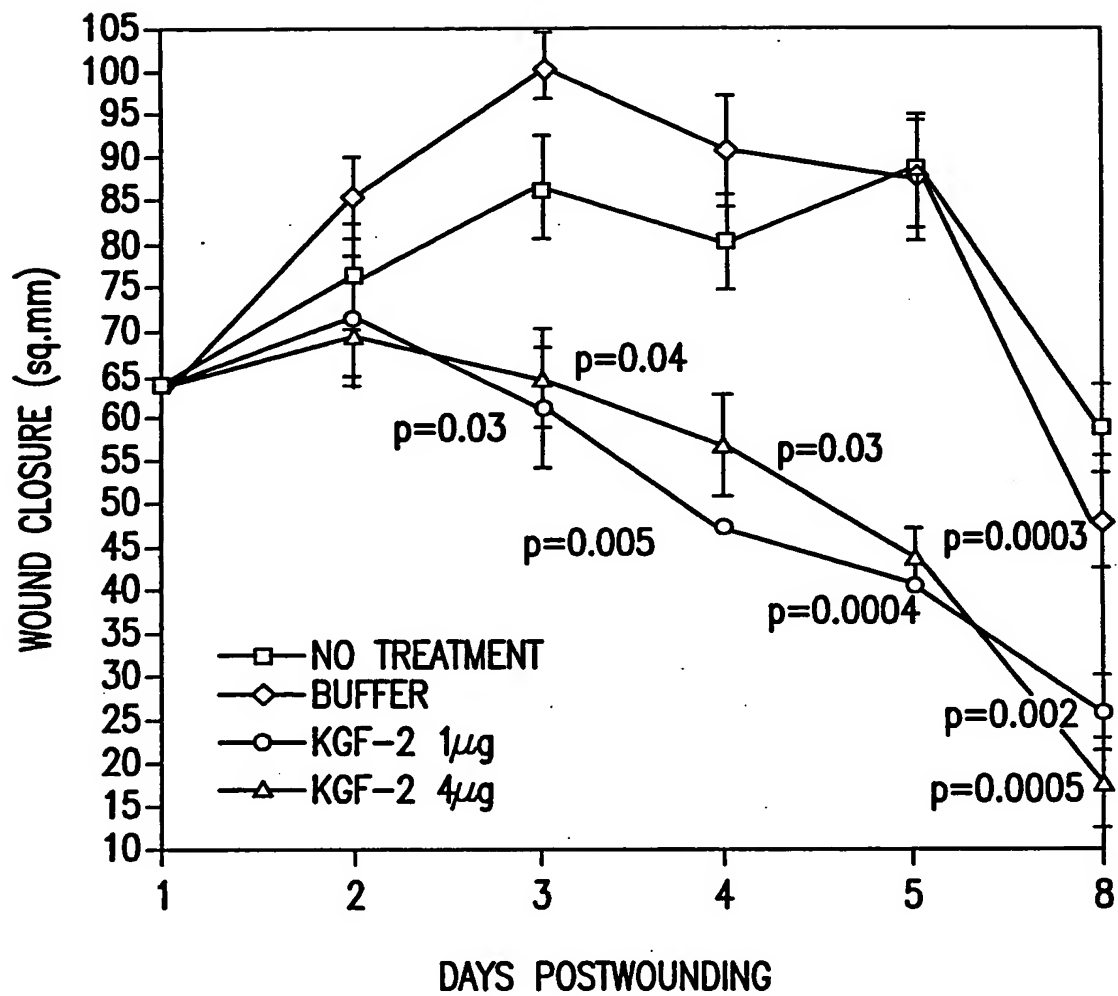


FIG.18

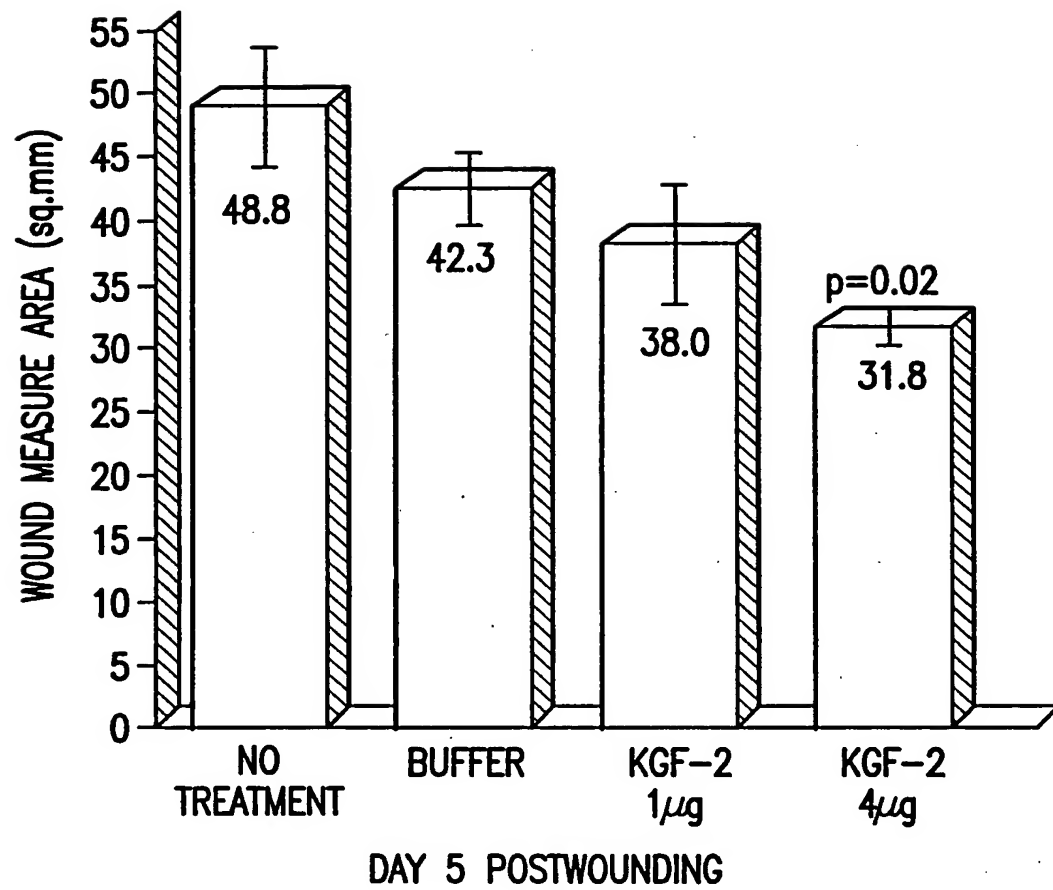
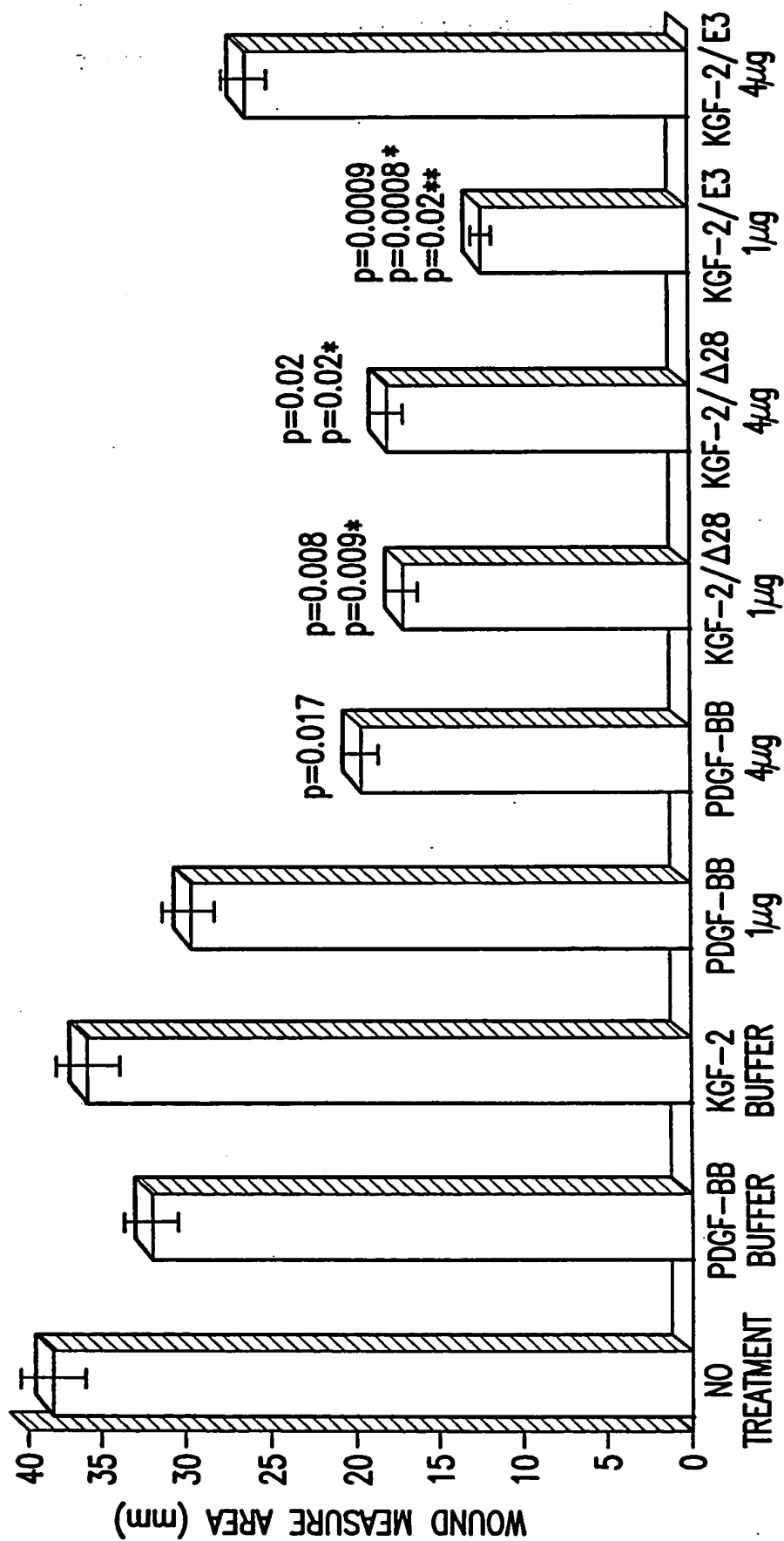


FIG.19A



DAY 10 POSTWOUNDING

FIG.19B

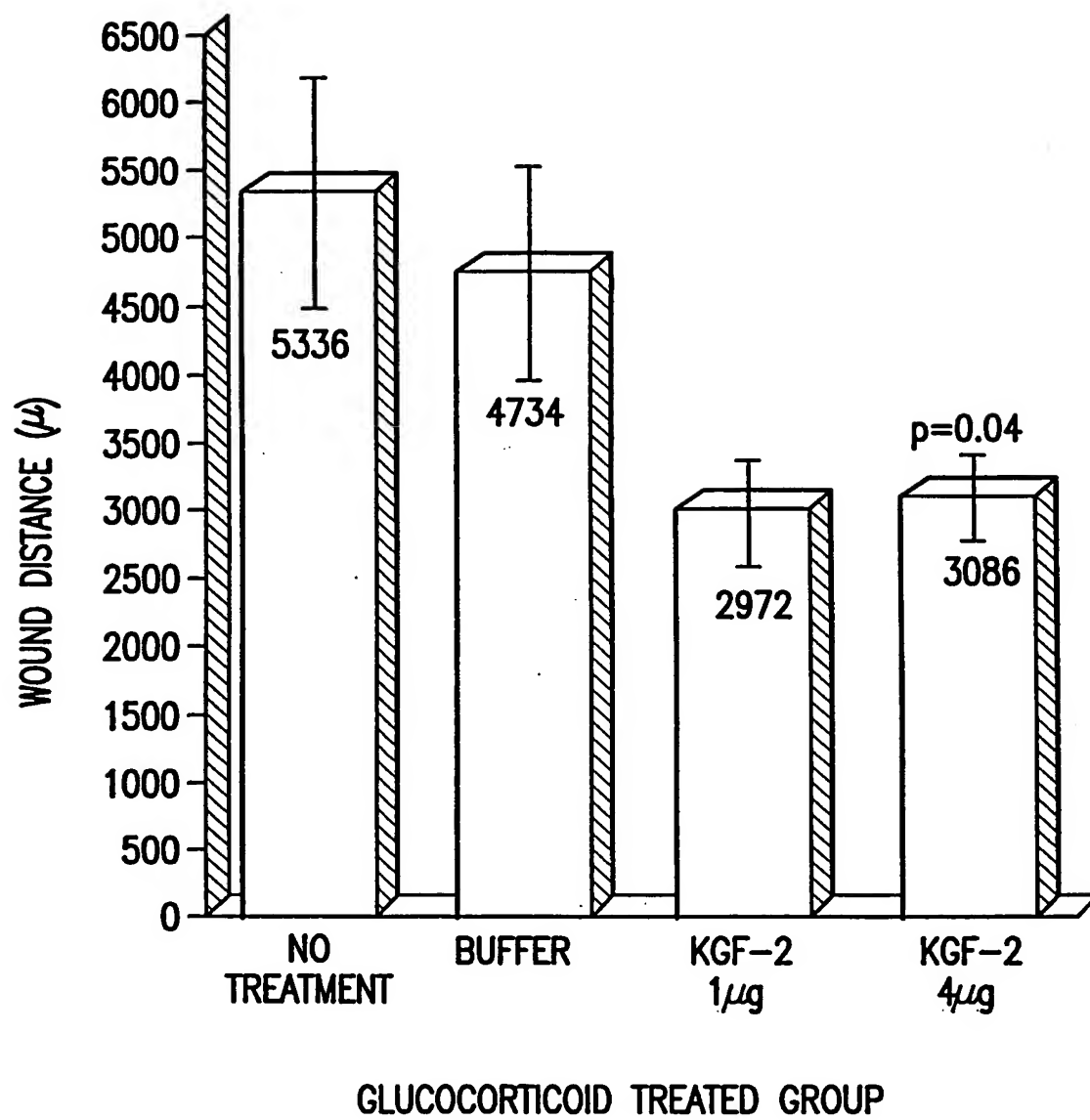


FIG.20

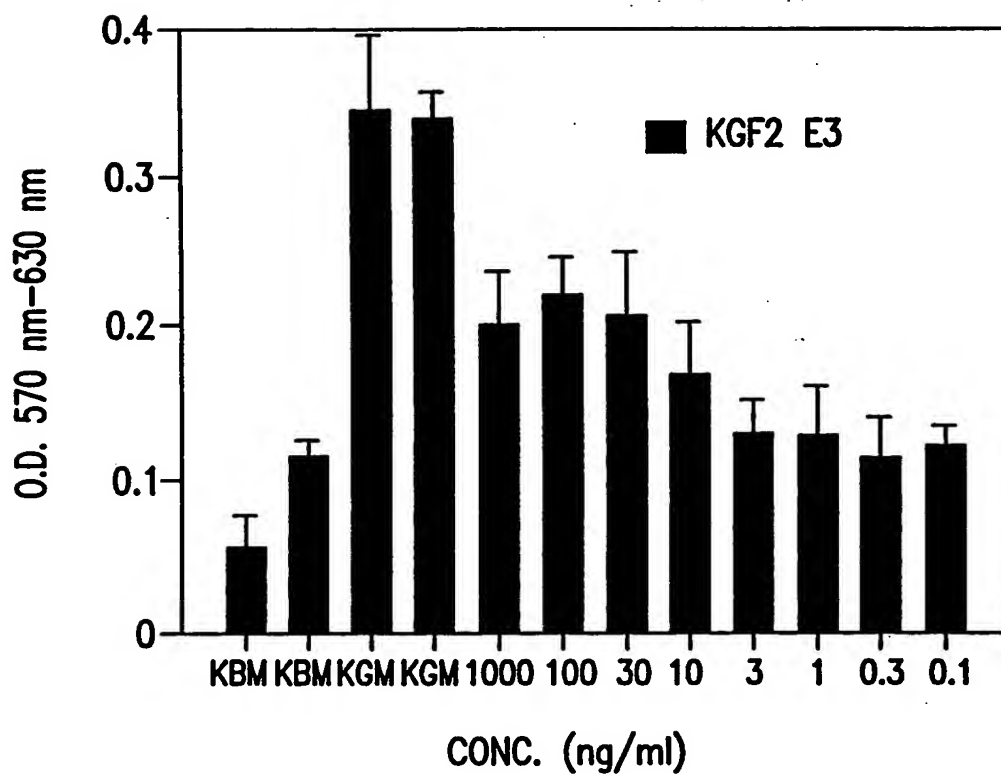


FIG.21A

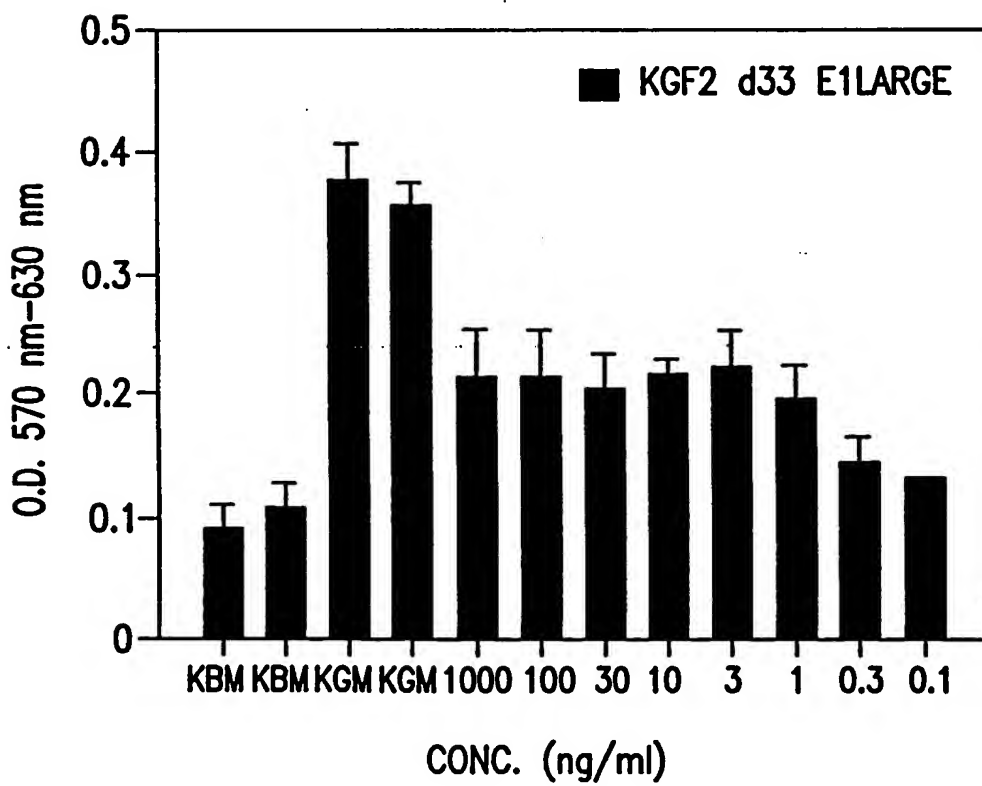


FIG.21B

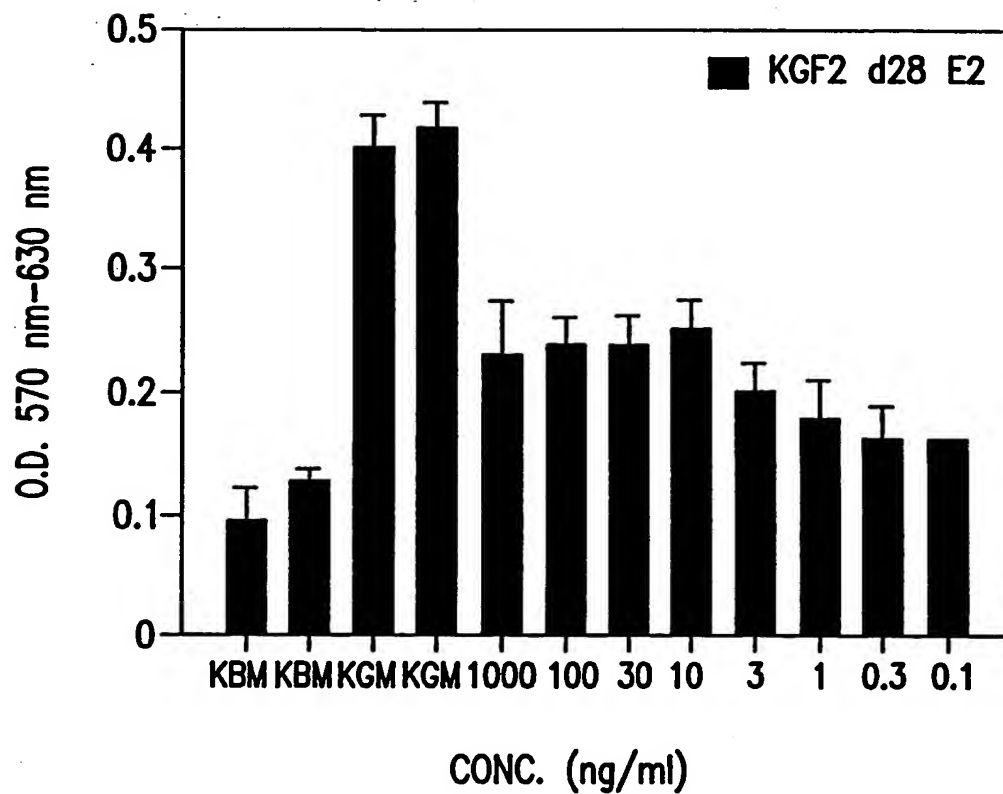


FIG.21C

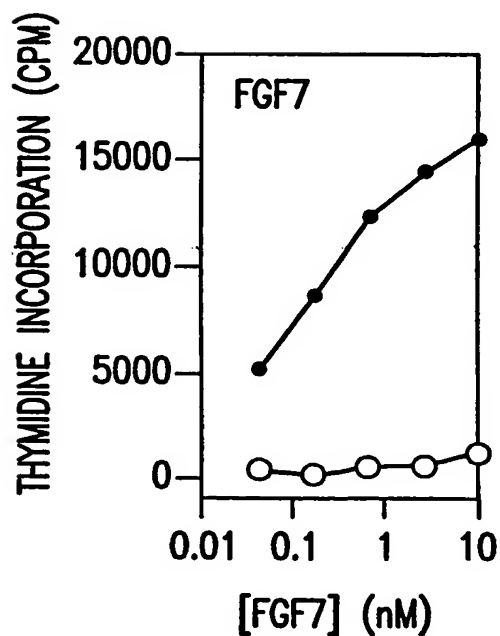


FIG.22A

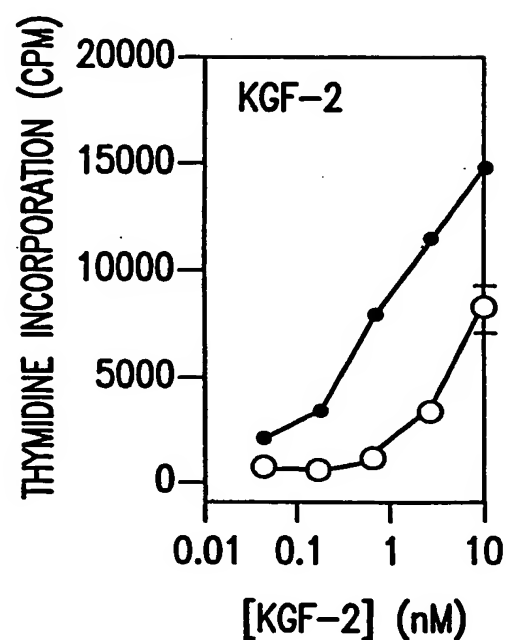


FIG.22A-1

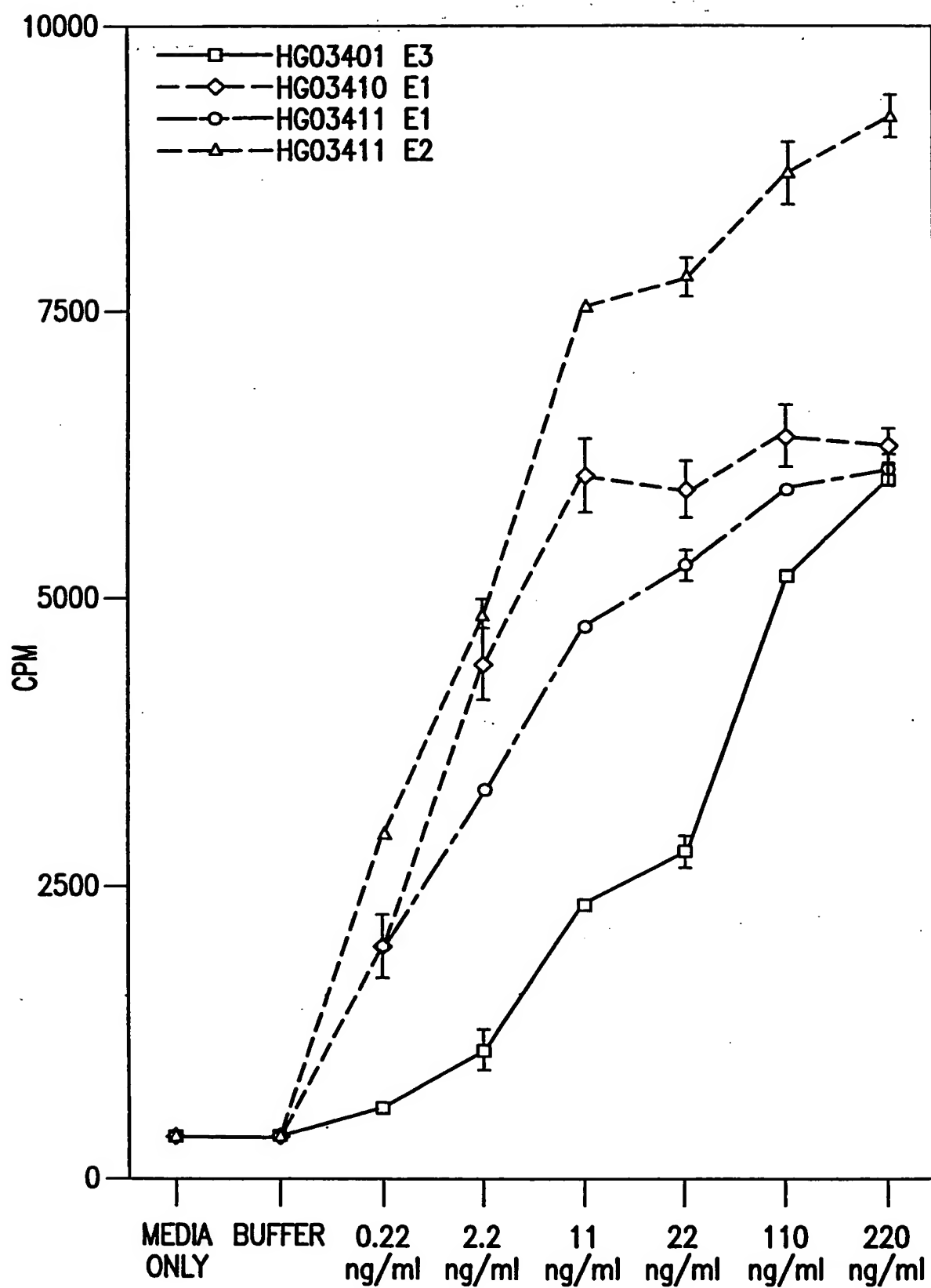


FIG.22B

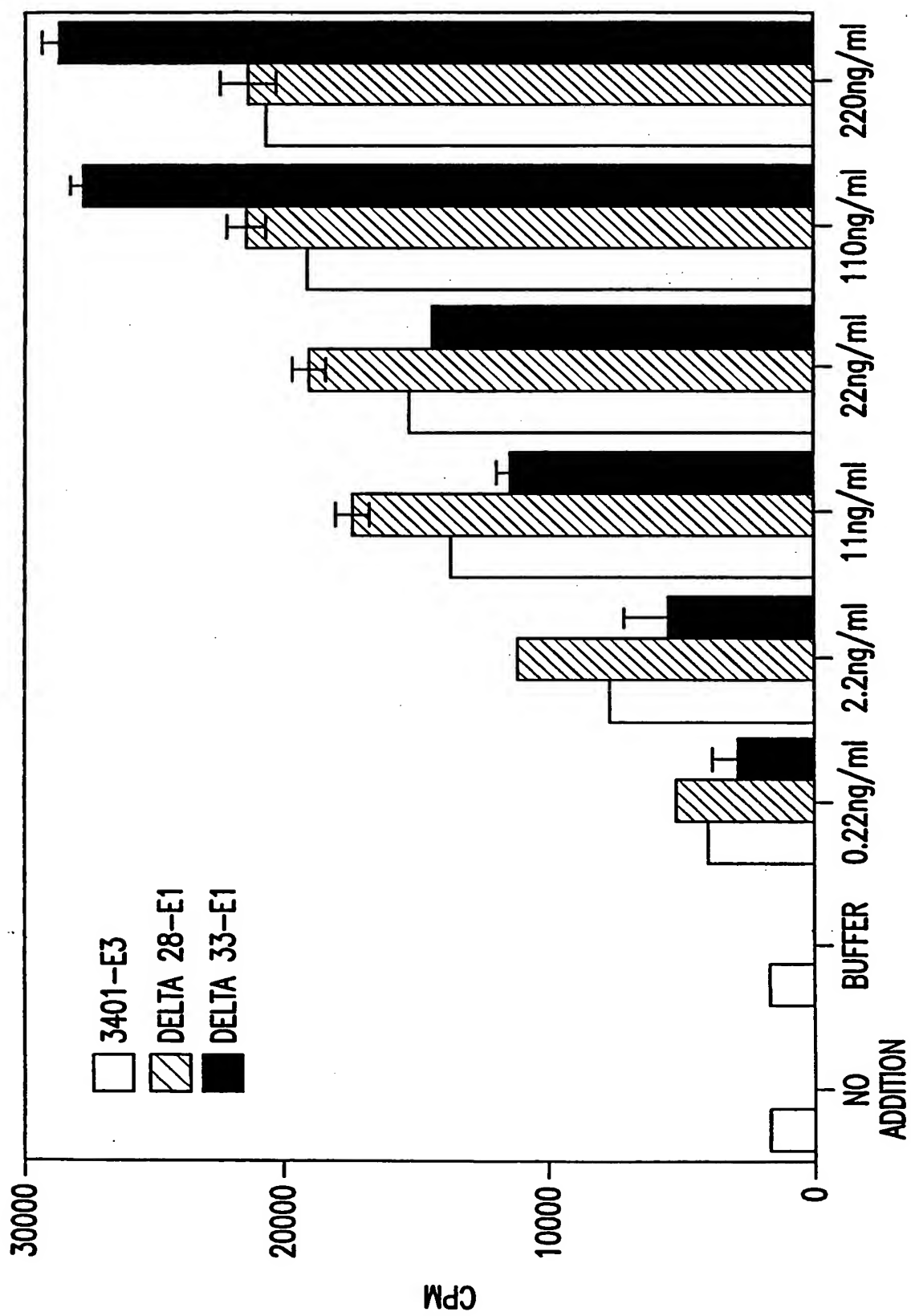


FIG.22C

ATGTGGAAATGGATACTGACCCACTGCGCTTCTGCTTTCCCGCACCTGCCGGGTGCTGC 60
 Met Trp Lys Trp Ile Leu Thr His Cys Ala Ser Ala Phe Pro His Leu Pro Gly Cys Cys
 |-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

TGCTGCTGCTTCCTGCTGCTGTTCTTCTGTTCCGGTTACCTGCCAGGCTCTG 120
 Cys Cys Cys Phe Leu Leu Leu Phe Leu Val Ser Ser Val Pro Val Thr Cys Gln Ala Leu
 |-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

GGTCAGGACATGGTTTCTCCGGAAGCTACCAACTCTTCCTCTTCTTTCTTTCCCCG 180
 Gly Gln Asp Met Val Ser Pro Glu Ala Thr Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro
 |-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

ACTTCCGCTGGTCGTCACGTTTCGTTCTTACAACCACCTGCAGGGTGACGTTTCGTTGGCGT 240
 Thr Ser Ala Gly Arg His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg
 |-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

AAAGTGTCTCTTTACCAAATACTTCCTGAAAATCGAAAAAACGGTAAAGTTTCTGGG 300
 Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val Ser Gly
 |-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

ACCAAGAAGGAGAACTGCCCGTACAGCATCCTGGAGATAACATCAGTAGAAATCGGAGTT 360
 Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser Val Glu Ile Gly Val
 |-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

GTTGCCGTCAAAGCCATTAACAGCAACTATTACTTAGCCATGAACAAGAAGGGGAAACTC 420
 Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu
 |-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

TATGGCTCAAAGAATTTAACAATGACTGTAAGCTGAAGGAGAGGATAGAGGAAAATGGA 480
 Tyr Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly
 |-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

TACAATACCTATGCATCATTTAACTGGCAGCATAATGGGAGGCAAATGTATGTGGCATTG 540
 Tyr Asn Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala Leu
 |-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

AATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAACACGAAGGAAAAACACCTCTGCTCAC 600
 Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg Lys Asn Thr Ser Ala His
 |-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

TTTCTTCCAATGGTGGTACACTCATAG 627
 Phe Leu Pro Met Val Val His Ser *
 |-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

FIG 23

ATGACCTGCCAGGCTCTGGGTCAGGACATGGTTTCTCCGGAAGCTACCAACTCTTCCTCT	60
MetThrCysGlnAlaLeuGlyGlnAspMetValSerProGluAlaThrAsnSerSerSer	
TCCTCTTTCTCTTCCCCGCTTCCGCTGGTCGTCACGTTTCGTTCTTACAACCACCTGCAG	120
SerSerPheSerSerProSerSerAlaGlyArgHisValArgSerTyrAsnHisLeuGln	
GGTGACGTTTCGTTGGCGTAACTGTTCTCTTTCACCAAATACTTCCTGAAAATCGAAAAA	180
GlyAspValArgTrpArgLysLeuPheSerPheThrLysTyrPheLeuLysIleGluLys	
AACGGTAAAGTTTCTGGGACCAAGAAGGAGAACTGCCCGTACAGCATCCTGGAGATAACA	240
AsnGlyLysValSerGlyThrLysLysGluAsnCysProTyrSerIleLeuGluIleThr	
TCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAAACAGCAACTATTACTTAGCCATG	300
SerValGluIleGlyValValAlaValLysAlaIleAsnSerAsnTyrTyrLeuAlaMet	
AACAAGAAGGGGAAACTCTATGGCTCAAAGAATTTAACAATGACTGTAAGCTGAAGGAG	360
AsnLysLysGlyLysLeuTyrGlySerLysGluPheAsnAsnAspCysLysLeuLysGlu	
AGGATAGAGGAAAATGGATACAATACCTATGCATCATTTAACTGGCAGCATAATGGGAGG	420
ArgIleGluGluAsnGlyTyrAsnThrTyrAlaSerPheAsnTrpGlnHisAsnGlyArg	
CAATGTATGTGGCATTGAATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAACACGAAGG	480
GlnMetTyrValAlaLeuAsnGlyLysGlyAlaProArgArgGlyGlnLysThrArgArg	
AAAAACACCTCTGCTCACTTTCTTCCAATGGTGGTACACTCATAG	525
LysAsnThrSerAlaHisPheLeuProMetValValHisSer *	

FIG.24A

ATGACTTGCCAGGCACTGGGTCAAGACATGGTTTCCCGGAAGCTACCAACAGCTCCAGCTCTAGCTTCA
 |-----|-----|-----|-----|-----|-----|-----|-----|-----|-----| 70
 TACTGAACGGTCCGTGACCCAGTTCTGTACCAAAGGGCCTTCGATGGTTGTGAGGTGAGATCGAAGT
 M T C Q A L G Q D M V S P E A T N S S S S F
 |-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
 GCAGCCCATCTAGCGCAGGTGTCACGTTGCTCTTACAACCACTTACAGGGTGATGTTGTTGGCGCAA
 |-----|-----|-----|-----|-----|-----|-----|-----|-----|-----| 140
 CGTGGGTAGATCGGTCCAGCAGTGCAAGCGAGAATGTTGGTGAATGTCCCACTACAAGCAACCGCGTT
 S S P S S A G R H V R S Y N H L Q G D V R W R K
 |-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
 ACTGTTCACTTTACCAAGTACTTCTGAAAATCGAAAAACGGTAAAGTTTCTGGGACCAAGAAGGAG
 |-----|-----|-----|-----|-----|-----|-----|-----|-----|-----| 210
 TGACAAGTCGAAATGGTTCATGAAGGACTTTTAGCTTTTTTGGCATTTCAAAGACCTGGTTCCTCCTC
 L F S F T K Y F L K I E K N G K V S G T K K E
 |-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
 AACTGCCCGTACAGCATCCTGGAGATAACATCAGTAGAAATCGGAGTTGTTGCGTCAAAGCCATTAACA
 |-----|-----|-----|-----|-----|-----|-----|-----|-----|-----| 280
 TTGACGGGCATGTGTAGGACCTCTATTGTAGTCATCTTAGCCTCAACAACGGCAGTTTCGGTAATTGT
 N C P Y S I L E I T S V E I G V V A V K A I N
 |-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
 GCAACTATTACTTAGCCATGAACAAGAAGGGGAACTCTATGGCTCAAAGAATTTAACAATGACTGTAA
 |-----|-----|-----|-----|-----|-----|-----|-----|-----|-----| 350
 CGTTGATAATGAATCGGTACTTGTCTTCCCTTTGAGATACCGAGTTTCTTAAATTGTTACTGACATT
 S N Y Y L A M N K K G K L Y G S K E F N N D C K
 |-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
 GCTGAAGGAGAGGATAGAGGAAAATGGATACAATACCTATGCATCATTTAACTGCCAGCATAATGGGAGG
 |-----|-----|-----|-----|-----|-----|-----|-----|-----|-----| 420
 CGACTTCCTCTCCTATCTCCTTTTACCTATGTTATGGATACGTAGTAAATTGACCGTGTATTACCCCTCC
 L K E R I E E N G Y N T Y A S F N W Q H N G R
 |-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
 CAAATGTATGTGGCATTGAATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAACAGGAAGGAAAAACACCT
 |-----|-----|-----|-----|-----|-----|-----|-----|-----|-----| 490
 GTTTACATACACCGTAACCTTACCTTTTCTCGAGGTTCCTCTCCTGTCTTTTGTGCTTCCTTTTGTGGA
 Q M Y V A L N G K G A P R R G Q K T R R K N T
 |-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
 CTGCTCACTTTCTTCCAATGGTGGTACACTCATAG
 |-----|-----|-----|-----|-----|-----|-----|-----|-----|-----| 525
 GACGAGTGAAAGAAGGTTACCACCATGTGAGTATC
 S A H F L P M V V H S
 |-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

FIG 24B

ATGACCTGCCAGGCTCTGGGTCAGGACATGGTTTCTCCGGAAGCTACCAACTCTTCC
TCTTCCTCTTTCTCTTCCCCGTCTTCGCTGGTCGTCACGTTGTTCTTACAACCAC
CTGCAGGGTGACGTTGTTGGCGTAAACTGTTCTCTTTCACCAAATACTTCCTGAAA
ATCGAAAAAACGGTAAAGTTTCTGGGACCAAGAAGGAGAACTGCCCGTACAGCATC
CTGGAGATAACATCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAACAGCAAC
TATTACTTAGCCATGAACAAGAAGGGGAAACTCTATGGCTCAAAGAATTAAACAAT
GACTGTAAGCTGAAGGAGAGGATAGAGGAAAATGGATACAATACCTATGCATCATTT
AACTGGCAGCATAATGGGAGGCAAATGTATGTGGCATTGAATGGAAAAGGAGCTCCA
AGGAGAGGACAGAAAACACGAAGGAAAAACACCTCTGCTCACTTTCTTCCAATGGTG
GTACACTCATAG

MTCQALGQDMVSPEATNSSSSSFSSPSSAGRHVRSYNHLQGDVWRKLFSTKYFLKIE
KNGKVSGETTKENCPYSILEITSVEIGVVAVKAINSNYLAMNKKGKLYGSKEFNNDCKL
KERIEENGYNTYASFNWQHNGRQMYVALNGKGAPRRGQKTRRKNTSAHFLPMVVHS.

FIG.25

ATGGCTGGTCGTCACGTTGTTCTTACAACCACCTGCAGGGTGACGTTGTTGGCGT
AAACTGTTCTCTTTCACCAAATACTTCCTGAAAATCGAAAAAACGGTAAAGTTTCT
GGGACCAAGAAGGAGAACTGCCCGTACAGCATCCTGGAGATAACATCAGTAGAAATC
GGAGTTGTTGCCGTCAAAGCCATTAACAGCAACTATTACTTAGCCATGAACAAGAAG
GGGAAACTCTATGGCTCAAAGAATTAAACAATGACTGTAAGCTGAAGGAGAGGATA
GAGGAAAATGGATACAATACCTATGCATCATTTAACTGGCAGCATAATGGGAGGCAA
ATGTATGTGGCATTGAATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAACACGAAGG
AAAAACACCTCTGCTCACTTTCTTCCAATGGTGGTACACTCATAG

MAGRHVRSYNHLQGDVWRKLFSTKYFLKIEKNGKVSGETTKENCPYSILEITSVEIGV
VAVKAINSNYLAMNKKGKLYGSKEFNNDCKLKERIEENGYNTYASFNWQHNGRQMYVA
LNGKGAPRRGQKTRRKNTSAHFLPMVVHS.

FIG.26

ATGGTTCGTTGGCGTAACTGTTCTCTTTCACCAAATACTTCCTGAAAATCGAAAA
AACGGTAAAGTTTCTGGGACCAAGAAGGAGAACTGCCCGTACAGCATCCTGGAGATA
ACATCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAACAGCAACTATTACTTA
GCCATGAACAAGAAGGGGAACTCTATGGCTCAAAGAATTTAACAATGACTGTAAG
CTGAAGGAGAGGATAGAGGAAAATGGATACAATACCTATGCATCATTTAACTGGCAG
CATAATGGGAGGCAAATGTATGTGGCATTGAATGGAAAAGGAGCTCCAAGGAGAGGA
CAGAAAACACGAAGGAAAAACACCTCTGCTCACTTTCTTCCAATGGTGGTACACTCA
TAG

MVRWRKLSFTKYFLKIEKNGKVS GTKKENCPYSILEITSVEIGVVAVKAINS NYYLAM
NKKGKLYGSKEFNNDCKLKERIEENGYNTYASFNWQHNGRQMYVALNGKGAPRRGQKTR
RKNTSAHFLPMVVHS.

FIG.27

ATGGAAAAAACGGTAAAGTTTCTGGGACCAAGAAGGAGAACTGCCCGTACAGCAT
CCTGGAGATAACATCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAACAGCA
ACTATTACTTAGCCATGAACAAGAAGGGGAACTCTATGGCTCAAAGAATTTAAC
AATGACTGTAAGCTGAAGGAGAGGATAGAGGAAAATGGATACAATACCTATGCATC
ATTTAACTGGCAGCATAATGGGAGGCAAATGTATGTGGCATTGAATGGAAAAGGAG
CTCCAAGGAGAGGACAGAAAACACGAAGGAAAAACACCTCTGCTCACTTTCTTCCA
ATGGTGGTACACTCATAG

MEKNGKVS GTKKENCPYSILEITSVEIGVVAVKAINS NYYLAMNKKGKLYGSKEFNND
CLKERIEENGYNTYASFNWQHNGRQMYVALNGKGAPRRGQKTRRKNTSAHFLPMVVH
S.

FIG.28

ATGGAGAACTGCCCCGTACAGCATCCTGGAGATAACATCAGTAGAAATCGGAGTTGT
TGCCGTCAAAGCCATTAACAGCAACTATTACTTAGCCATGAACAAGAAGGGGAAAC
TCTATGGCTCAAAGAATTTAACAATGACTGTAAGCTGAAGGAGAGGATAGAGGAA
AATGGATAACAATACCTATGCATCATTTAACTGGCAGCATAATGGGAGGCAAATGTA
TGTGGCATTGAATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAACACGAAGGAAAA
ACACCTCTGCTCACTTTCTTCCAATGGTGGTACACTCATAG

MENCPYSILEITSVEIGVVAVKAINSNYLAMNKKGKLYGSKEFNNDCKLKERIEENGY
NTYASFNWQHNGRQMYVALNGKGAPRRGQKTRRKNTSAHFLPMVVHS.

FIG.29

ATGGTCAAAGCCATTAACAGCAACTATTACTTAGCCATGAACAAGAAGGGGAACT
CTATGGCTCAAAGAATTTAACAATGACTGTAAGCTGAAGGAGAGGATAGAGGAAA
ATGGATAACAATACCTATGCATCATTTAACTGGCAGCATAATGGGAGGCAAATGTAT
GTGGCATTGAATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAACACGAAGGAAAA
CACCTCTGCTCACTTTCTTCCAATGGTGGTACACTCATAG

MVKAINSNYLAMNKKGKLYGSKEFNNDCKLKERIEENGYNTYASFNWQHNGRQMY
VALNGKGAPRRGQKTRRKNTSAHFLPMVVHS.

FIG.30

ATGGGGAACTCTATGGCTCAAAGAATTTAACAATGACTGTAAGCTGAAGGAGAG
GATAGAGGAAAATGGATAACAATACCTATGCATCATTTAACTGGCAGCATAATGGGA
GGCAAATGTATGTGGCATTGAATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAACA
CGAAGGAAAAACACCTCTGCTCACTTTCTTCCAATGGTGGTACACTCATAG

MGKLYGSKEFNNDCKLKERIEENGYNTYASFNWQHNGRQMYVALNGKGAPRRGQKT
RRKNTSAHFLPMVVHS.

FIG.31

ATGACCTGCCAGGCTCTGGGTCAGGACATGGTTTCTCCGGAAGCTACCAACTCTTCC
TCTTCCTCTTTCTCTTCCCCGTCTTCCGCTGGTCGTCACGTTCTTACAACCAC
CTGCAGGGTGACGTTCTGTTGGCGTAAACTGTTCTCTTTCACCAAATACTTCCTGAAA
ATCGAAAAAACGGTAAAGTTTCTGGGACCAAGAAGGAGAACTGCCCCGTACAGCATC
CTGGAGATAACATCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAACAGCAAC
TATTACTTAGCCATGAACAAGAAGGGGAACTCTATGGCTCAAAGAATTTAACAAT
GACTGTAAGCTGAAG

MTQALGQDMVSPEATNSSSSSFSSPSSAGRHVRSYNHLQGDVRWRKLFSTKYFLKIE
KNGKVSGETKKENCYPYSILEITSVEIGVVAVKAINSYYLAMNKKGKLYGSKEFNNDCKL
K

FIG.32

ATGGCTGGTCGTCACGTTCTTACAACCACCTGCAGGGTGACGTTCTGTTGGCGT
AAACTGTTCTCTTTCACCAAATACTTCCTGAAAATCGAAAAAACGGTAAAGTTTCT
GGGACCAAGAAGGAGAACTGCCCCGTACAGCATCCTGGAGATAACATCAGTAGAAATC
GGAGTTGTTGCCGTCAAAGCCATTAACAGCAACTATTACTTAGCCATGAACAAGAAG
GGGAAACTCTATGGCTCAAAGAATTTAACAATGACTGTAAGCTGAAG

MAGRHVRSYNHLQGDVRWRKLFSTKYFLKIEKNGKVSGETKKENCYPYSILEITSVEIGV
VAVKAINSYYLAMNKKGKLYGSKEFNNDCKLK

FIG.33

C-37 To Ser

ATGACCTCTCAGGCTCTGGGTCAGGACATGGTTTCTCCGGAAGCTACCAACTCTTCC
TCTTCCTCTTTCTCTTCCCGTCTTCCGCTGGTCGTACGTTCTTACAACCAC
CTGCAGGGTGACGTTTCGTTGGCGTAACTGTTCTCTTTCACCAAATACTTCCTGAAA
ATCGAAAAAACGGTAAAGTTTCTGGGACCAAGAAGGAGAACTGCCCGTACAGCATC
CTGGAGATAACATCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAAACAGCAAC
TATTACTTAGCCATGAACAAGAAGGGGAACTCTATGGCTCAAAGAATTTAACAAT
GACTGTAAGCTGAAGGAGAGGATAGAGGAAAATGGATACAATACCTATGCATCATTT
AACTGGCAGCATAATGGGAGGCAAATGTATGTGGCATTGAATGGAAAAGGAGCTCCA
AGGAGAGGACAGAAAACACGAAGGAAAAACACCTCTGCTCACTTTCTTCCAATGGTG
GTACACTCATAG

FIG.34

C-106 To Ser

ATGACCTGCCAGGCTCTGGGTCAGGACATGGTTTCTCCGGAAGCTACCAACTCTTCC
TCTTCCTCTTTCTCTTCCCGTCTTCCGCTGGTCGTACGTTCTTACAACCAC
CTGCAGGGTGACGTTTCGTTGGCGTAACTGTTCTCTTTCACCAAATACTTCCTGAAA
ATCGAAAAAACGGTAAAGTTTCTGGGACCAAGAAGGAGAACTCTCCGTACAGCATC
CTGGAGATAACATCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAAACAGCAAC
TATTACTTAGCCATGAACAAGAAGGGGAACTCTATGGCTCAAAGAATTTAACAAT
GACTGTAAGCTGAAGGAGAGGATAGAGGAAAATGGATACAATACCTATGCATCATTT
AACTGGCAGCATAATGGGAGGCAAATGTATGTGGCATTGAATGGAAAAGGAGCTCCA
AGGAGAGGACAGAAAACACGAAGGAAAAACACCTCTGCTCACTTTCTTCCAATGGTG
GTACACTCATAG

FIG.35

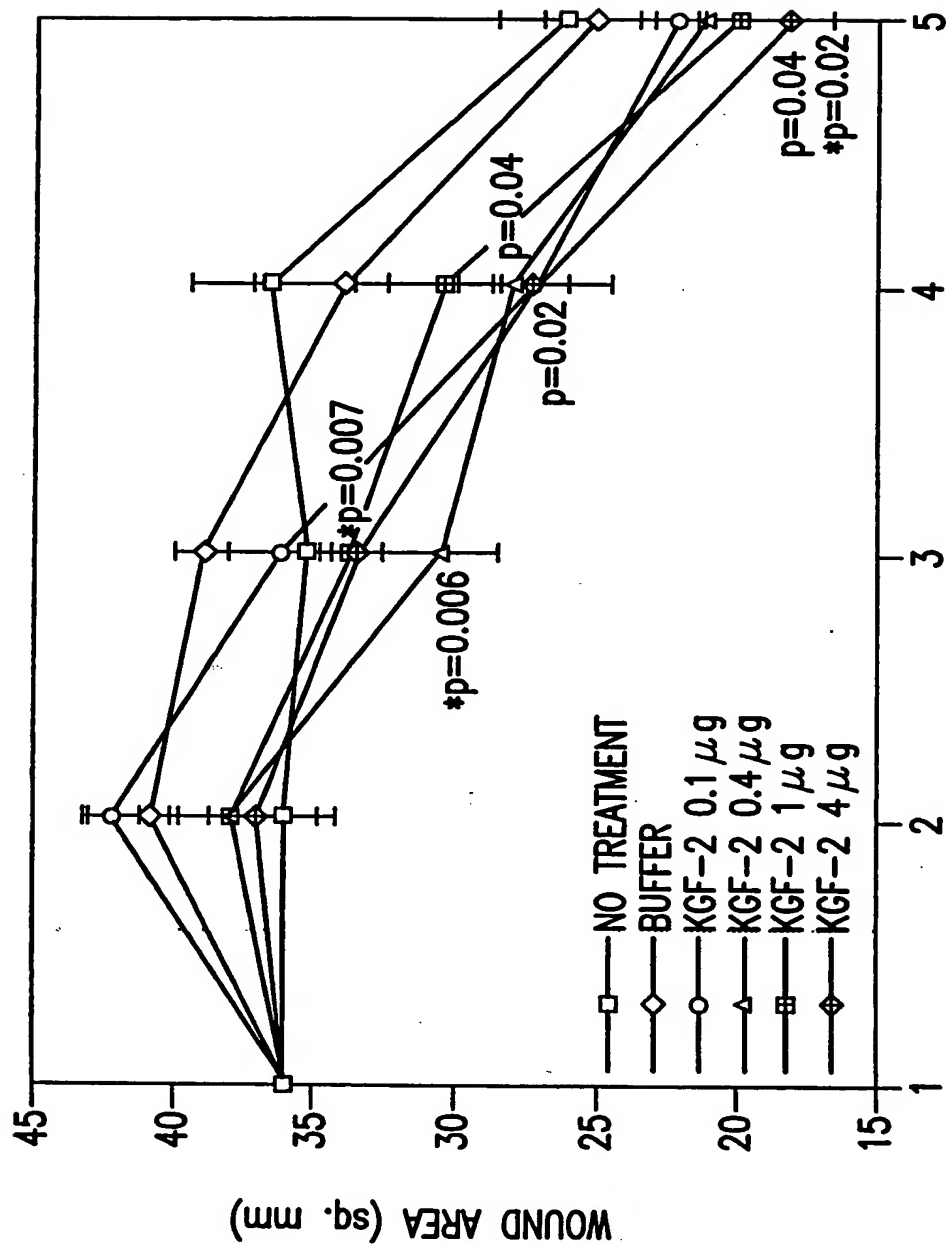


FIG.36

EFFECT OF KGF-2 $\Delta 33$ ON NORMAL WOUND HEALING RAT MODEL

TREATMENT GROUPS	WOUND SIZE (mm)	% WOUND CLOSURE	HISTOLOGICAL SCORE	RE-EPITH. (μm)	BrdU SCORE
NO TREATMENT	25.9 \pm 2.5	58.8 \pm 3.7	6.8 \pm 0.2	1142 \pm 141	3.8 \pm 0.4
BUFFER	25.1 \pm 1.7	60.2 \pm 2.6	6.4 \pm 0.2	923 \pm 61	5.0 \pm 0.4
KGF-2/ $\Delta 33$ (0.1 μg)	22.0 \pm 0.9	65 \pm 1.4	6.8 \pm 0.2	1275 \pm 148	4.6 \pm 0.7
KGF-2/ $\Delta 33$ (0.4 μg)	21.1 \pm 1.4	68.4 \pm 2.4	8.0 \pm 0.5 p=0.0445*	1310 \pm 182	4.2 \pm 0.7
KGF-2/ $\Delta 33$ (1.0 μg)	19.9 \pm 1.5	66.2 \pm 2.1	8.4 \pm 0.4 p=0.0159* p=0.0053†	1389 \pm 115 p=0.0074†	3.3 \pm 0.25 p=0.0217†
KGF-2/ $\Delta 33$ (4.0 μg)	18.1 \pm 1.6 p=0.0398* p=0.0200†	71.2 \pm 2.6 p=0.0367* p=0.0217†	8.5 \pm 0.3 p=0.0047* p=0.0445†	1220 \pm 89 p=0.0254†	5.3 \pm 0.9

FIG.37

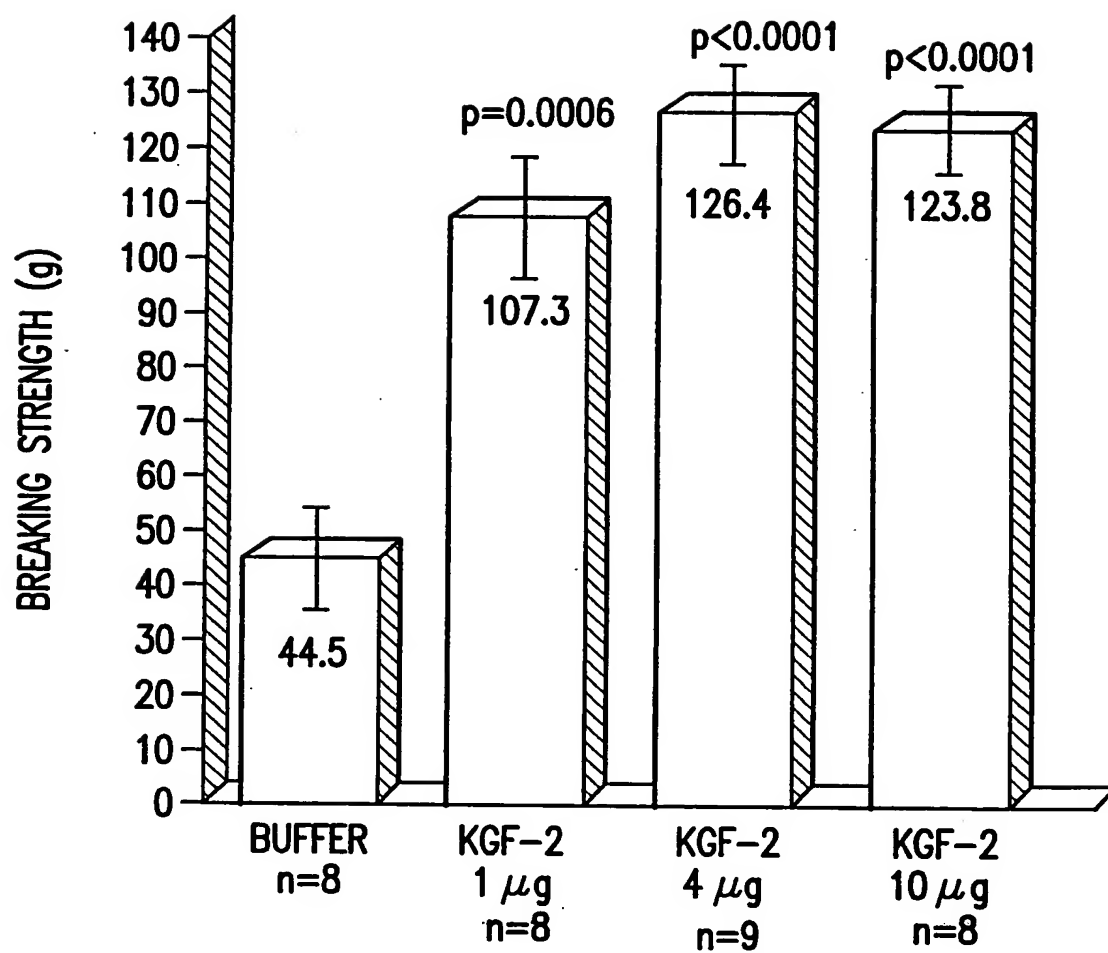


FIG.38

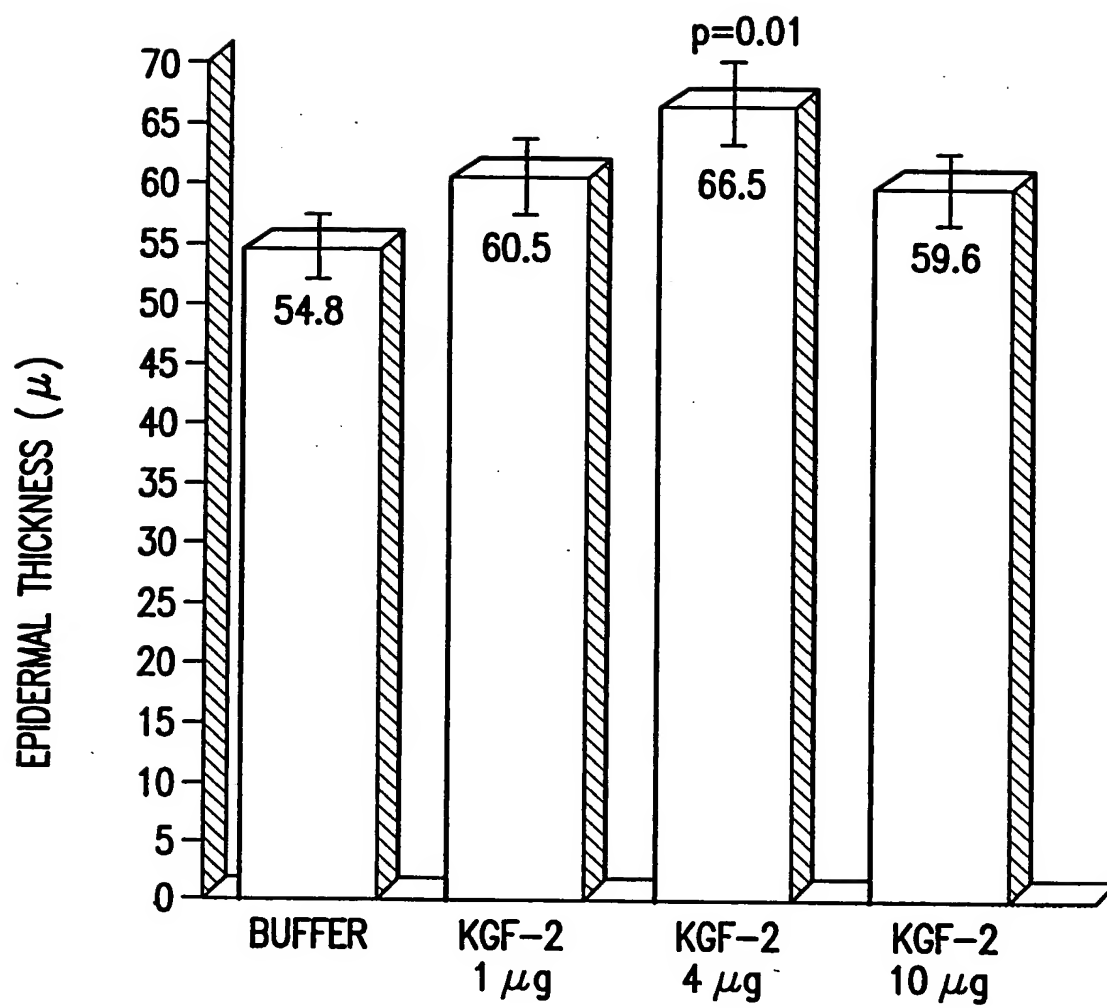


FIG.39

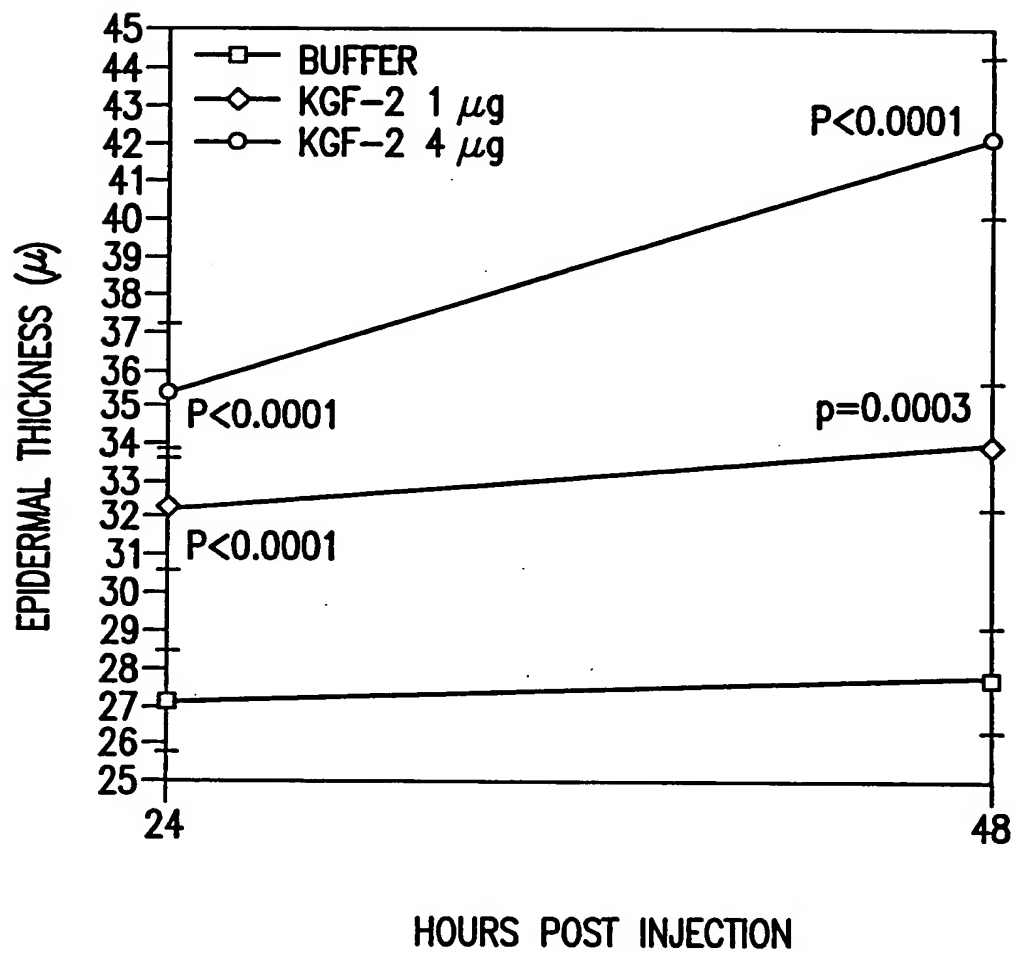


FIG.40

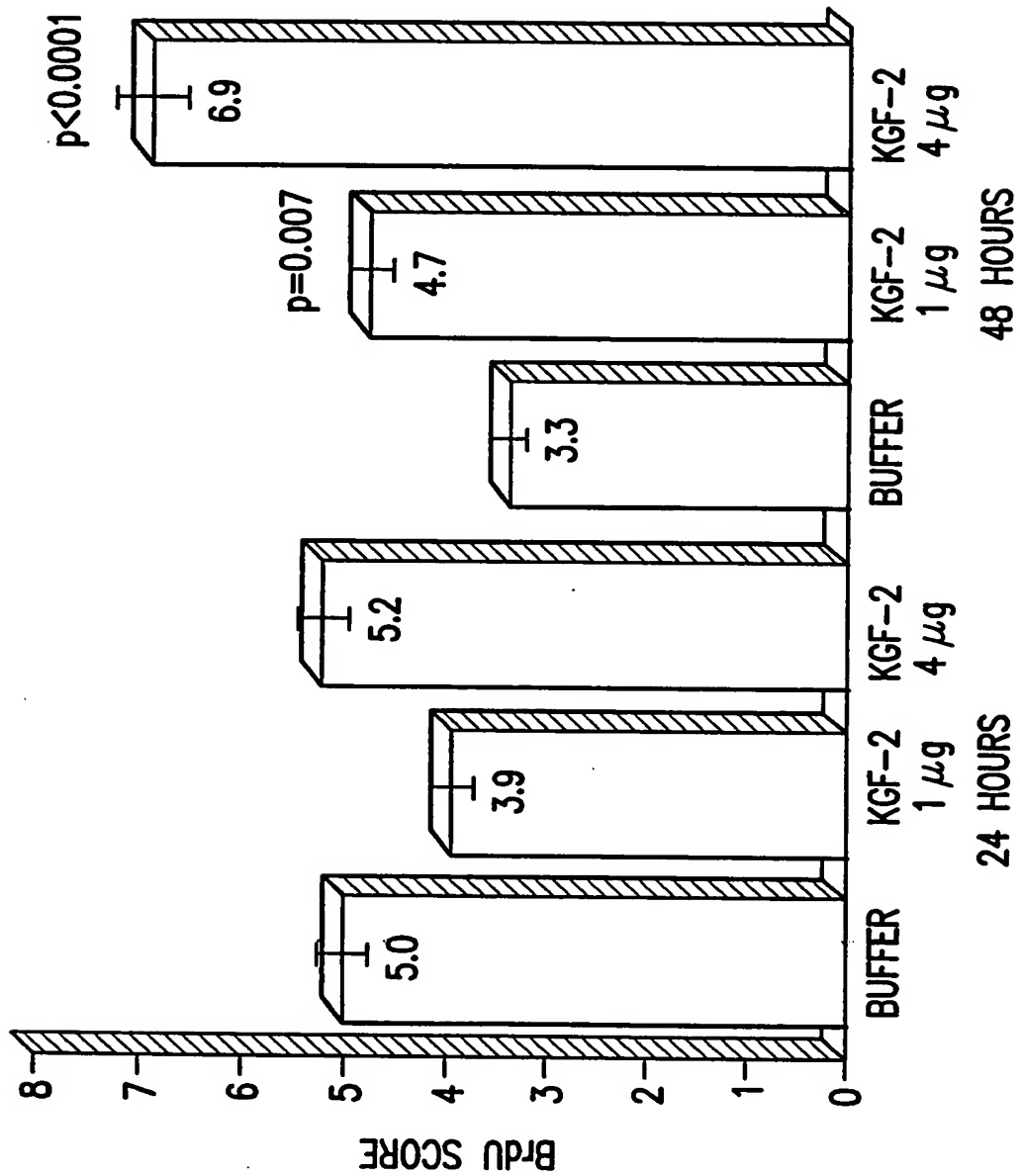


FIG.41

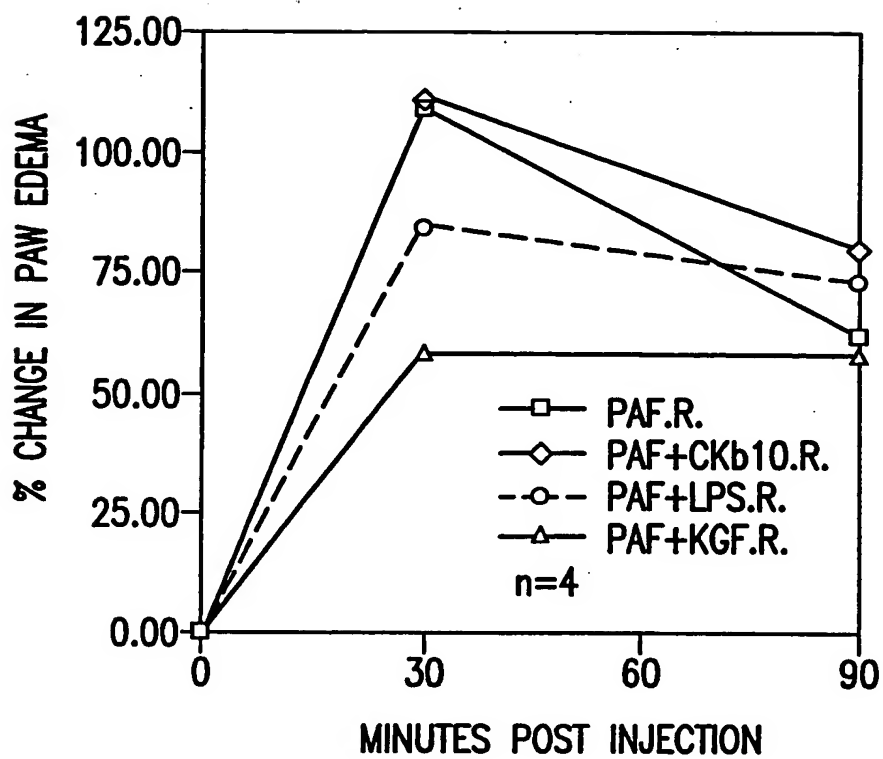


FIG.42A

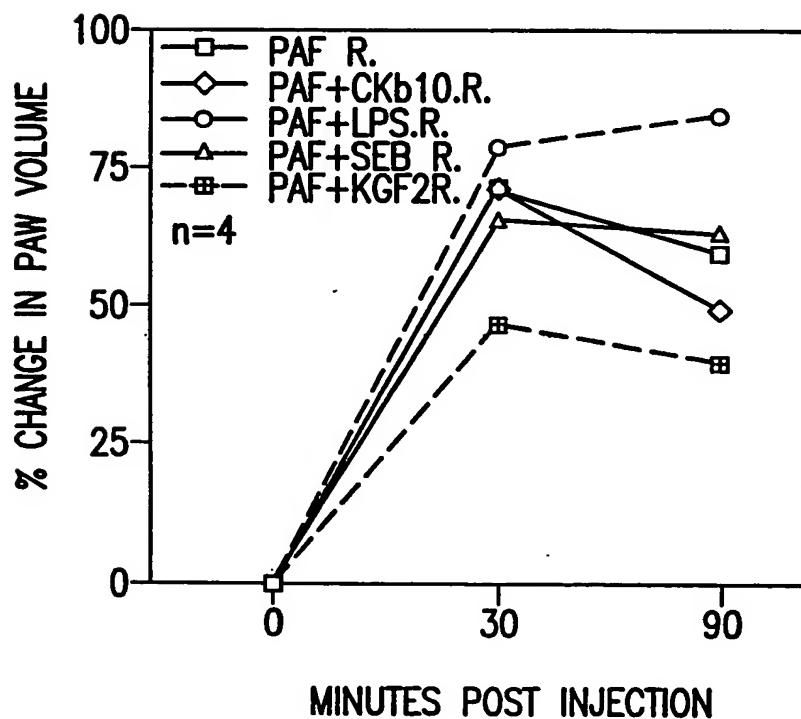


FIG.42B

EFFECT OF KGF-2 $\Delta 33$ ON PAF-INDUCED PAW EDEMA IN LEWIS RATS

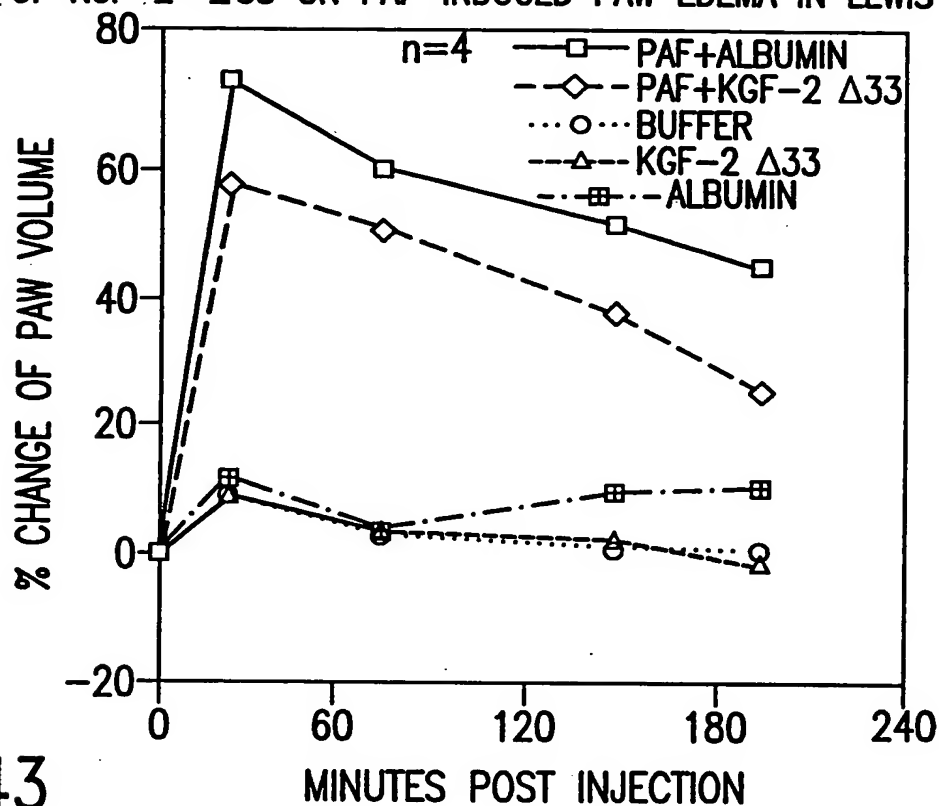


FIG.43

EFFECT OF KGF-2 $\Delta 33$ ON SURVIVAL OF WHOLE BODY IRRADIATED Balb/c MICE

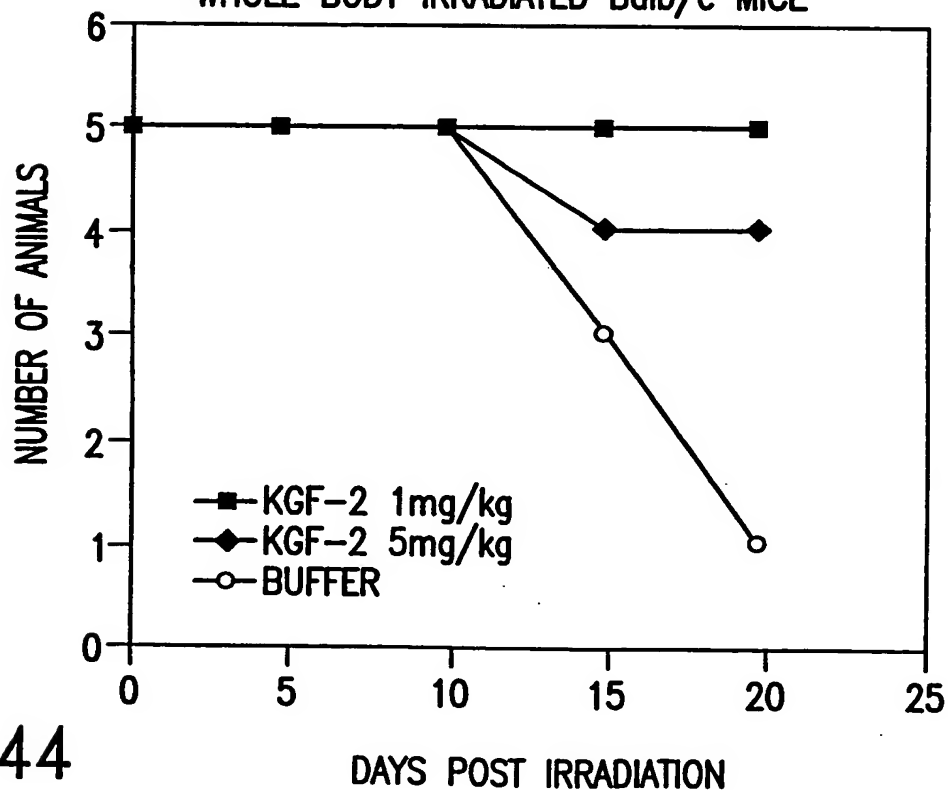


FIG 44

EFFECT OF KGF-2 $\Delta 33$ ON BODY WEIGHT OF IRRADIATED MICE

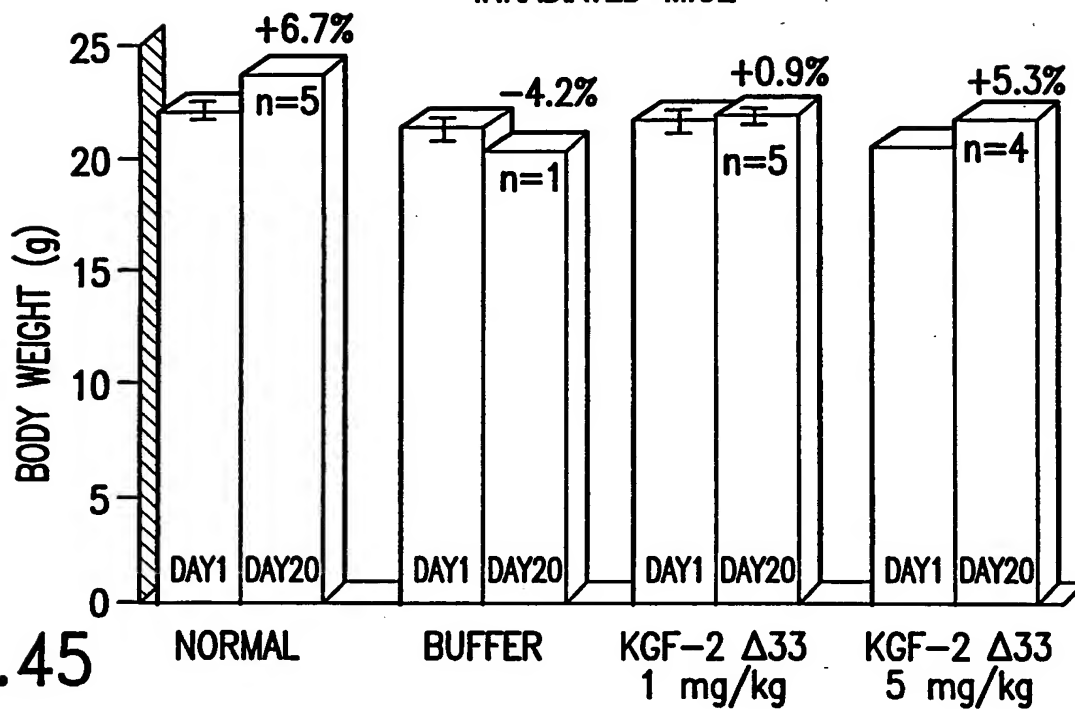
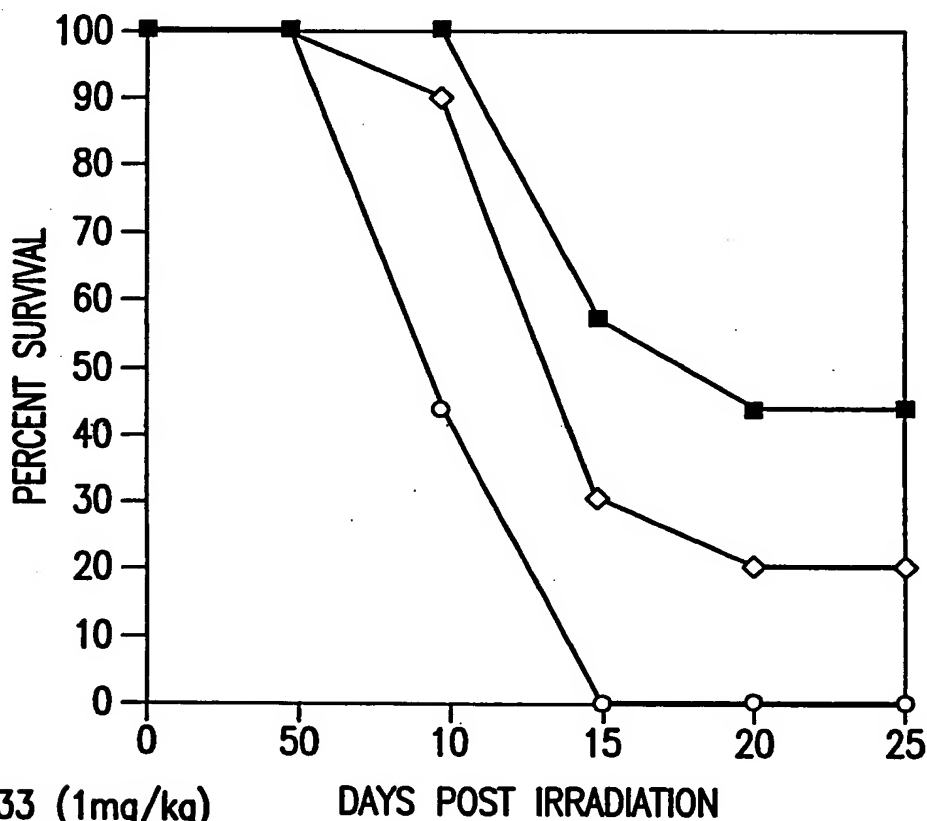


FIG.45



◇ KGF-2 $\Delta 33$ (1mg/kg)
 ■ KGF-2 $\Delta 33$ (5mg/kg)
 ○ BUFFER

FIG.46

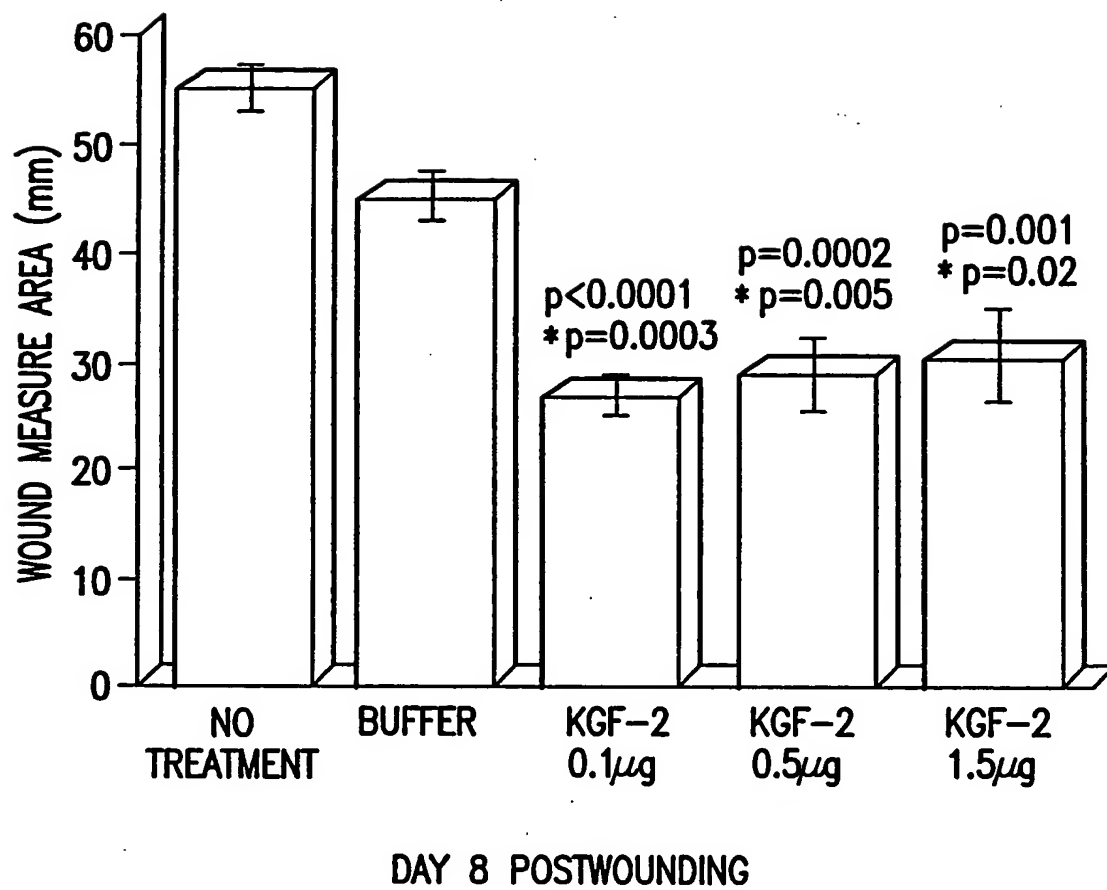


FIG.47

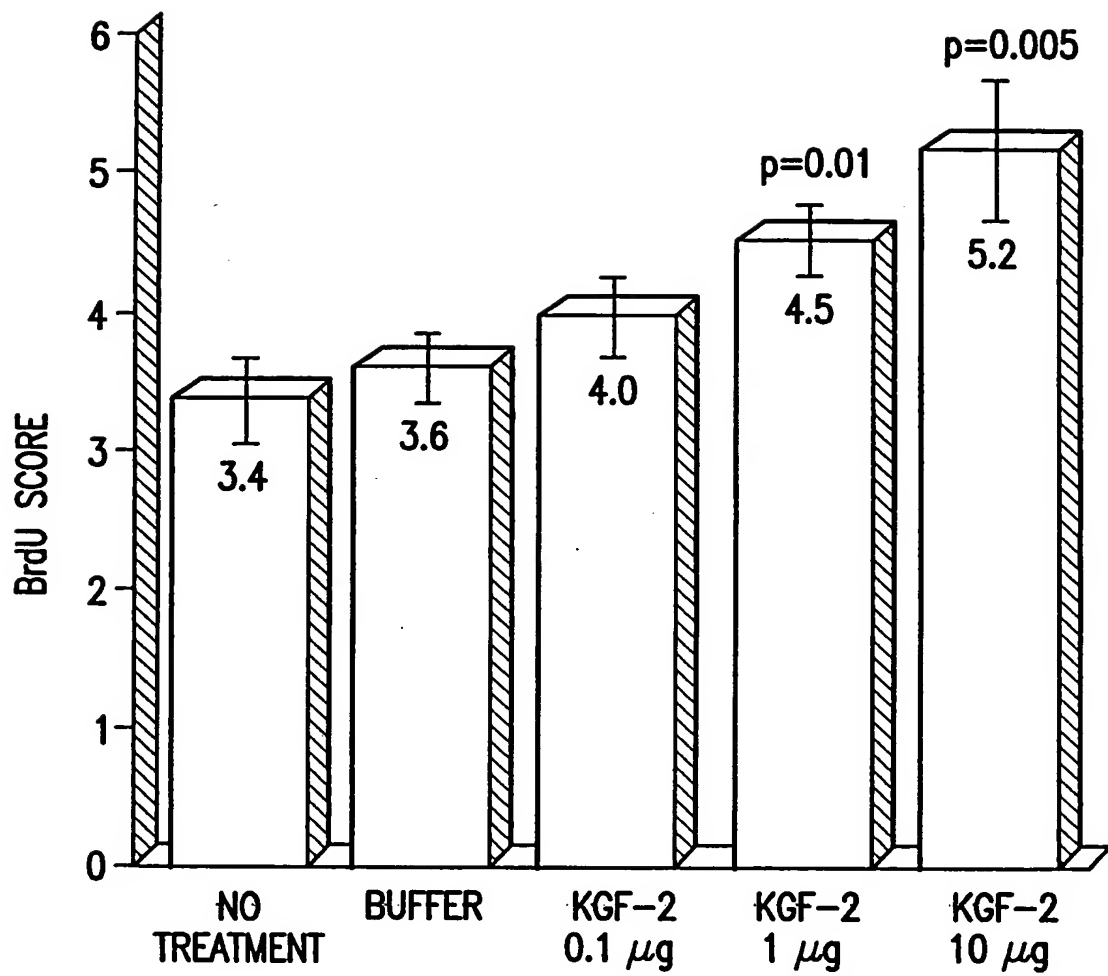


FIG.48

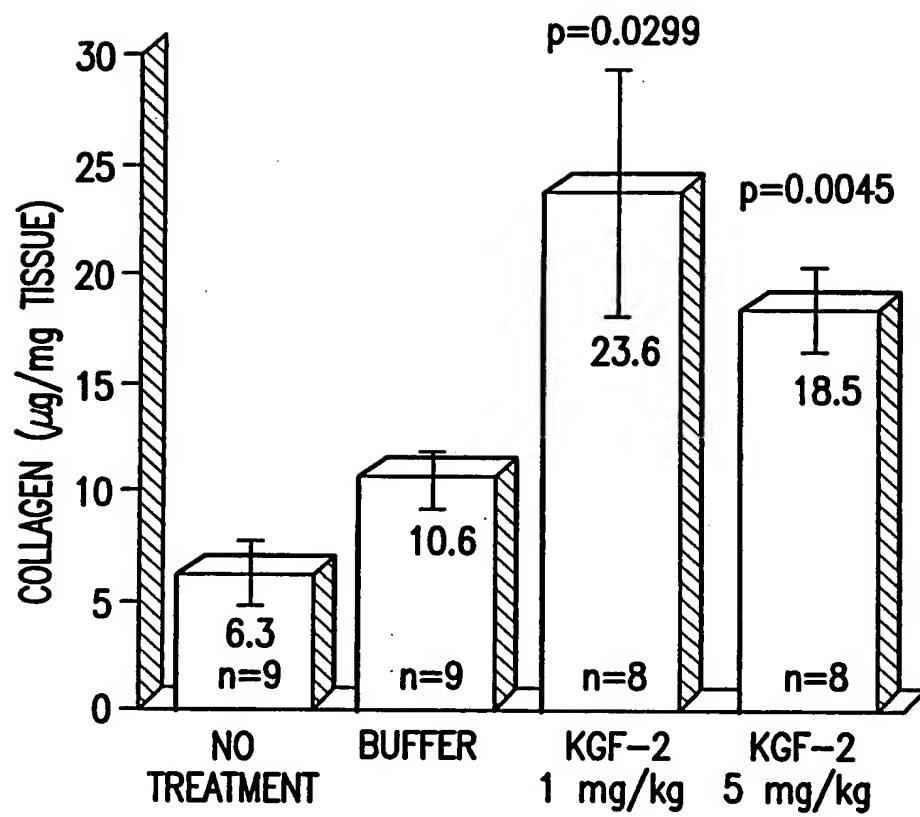


FIG.49

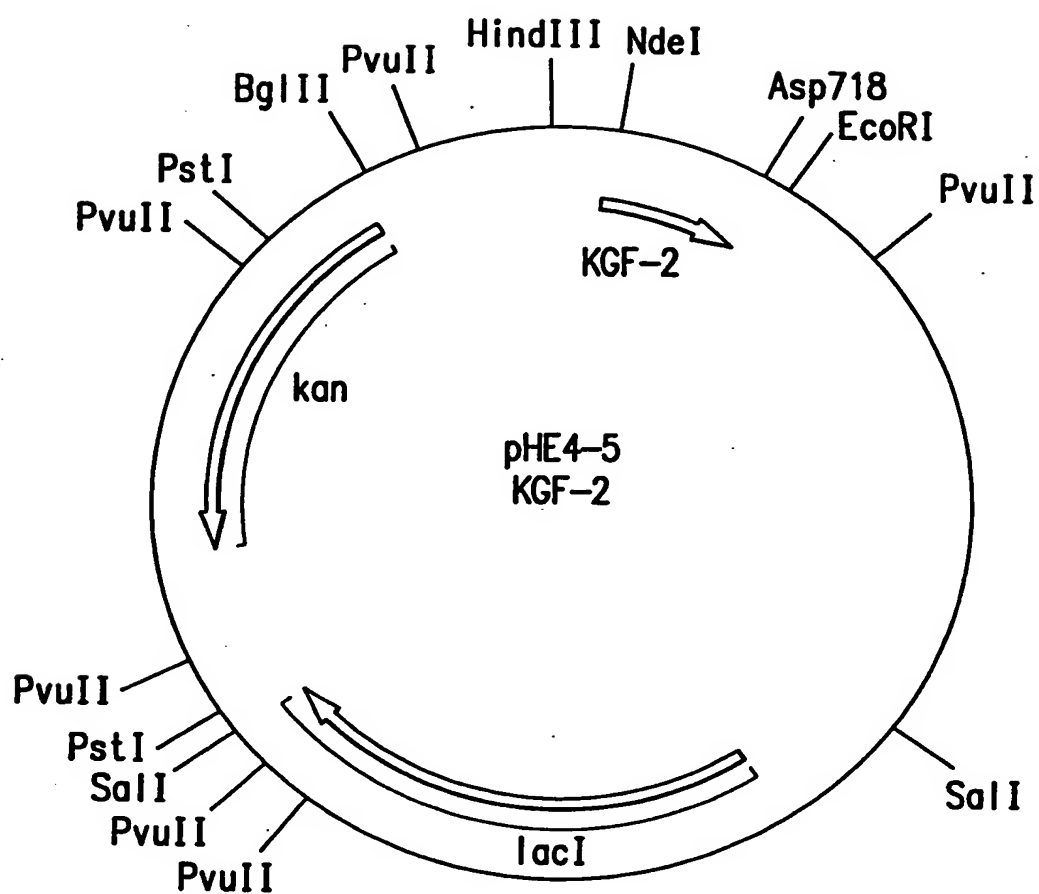


FIG.50

1 AAGCTTAAAAAAGTCAAAAAATAGT ⁻³⁵ TTGACT(TGTGAGCGGATAACAAT) Operator 1
 50 ⁻¹⁰ TAAGATGTACCCA ATTGTGAGCGGATAACAAT Operator 2 TTCACACATTAA
 94 ^{S/D} AGAGGAGAAATTA CATATG

FIG. 51

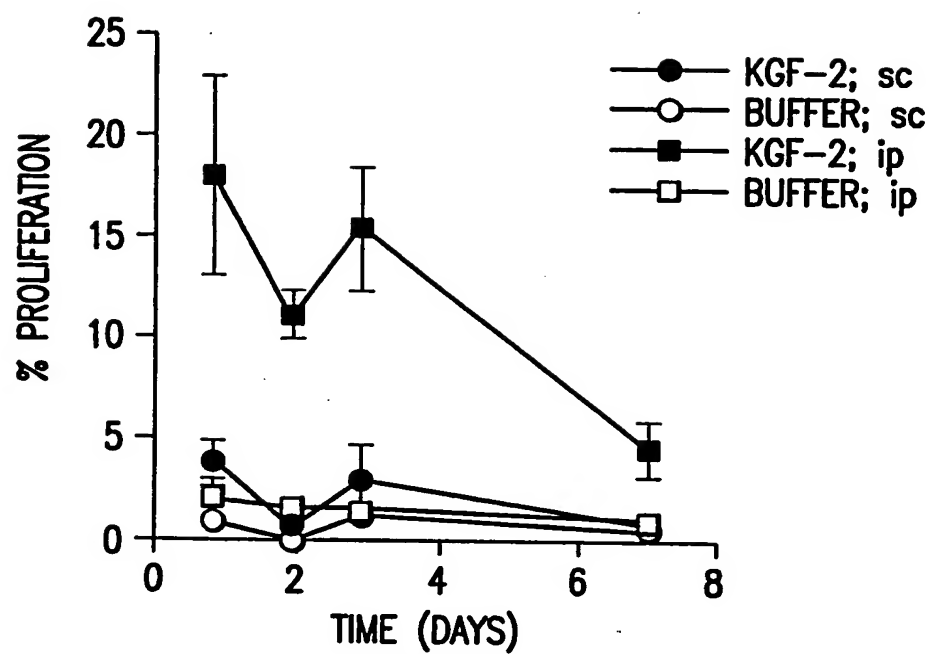


FIG. 52

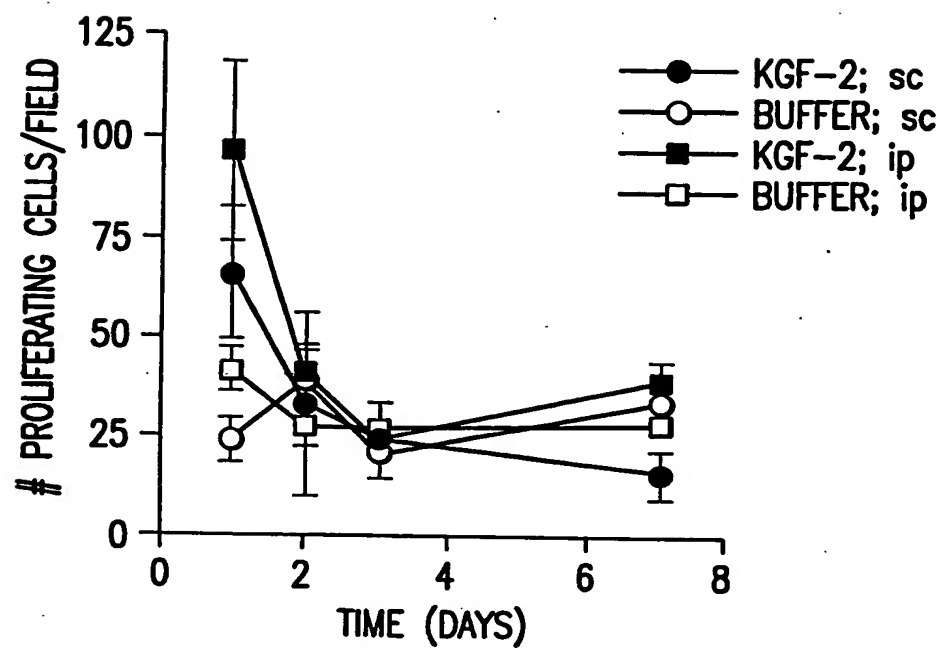


FIG. 53

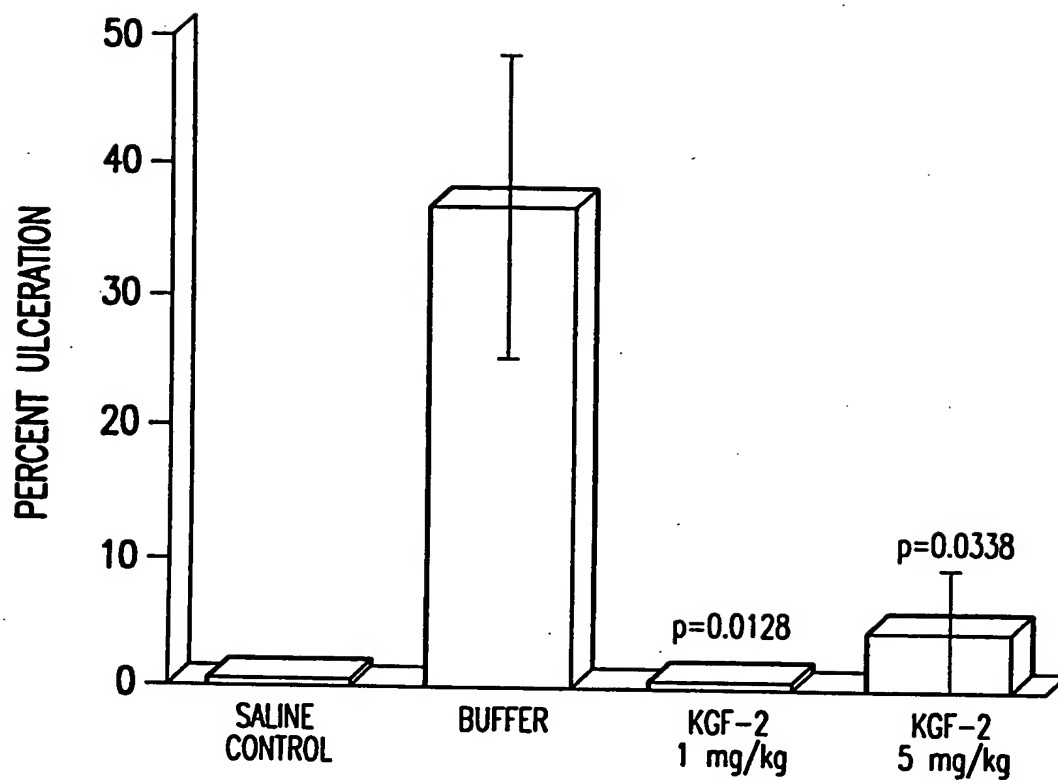


FIG. 54

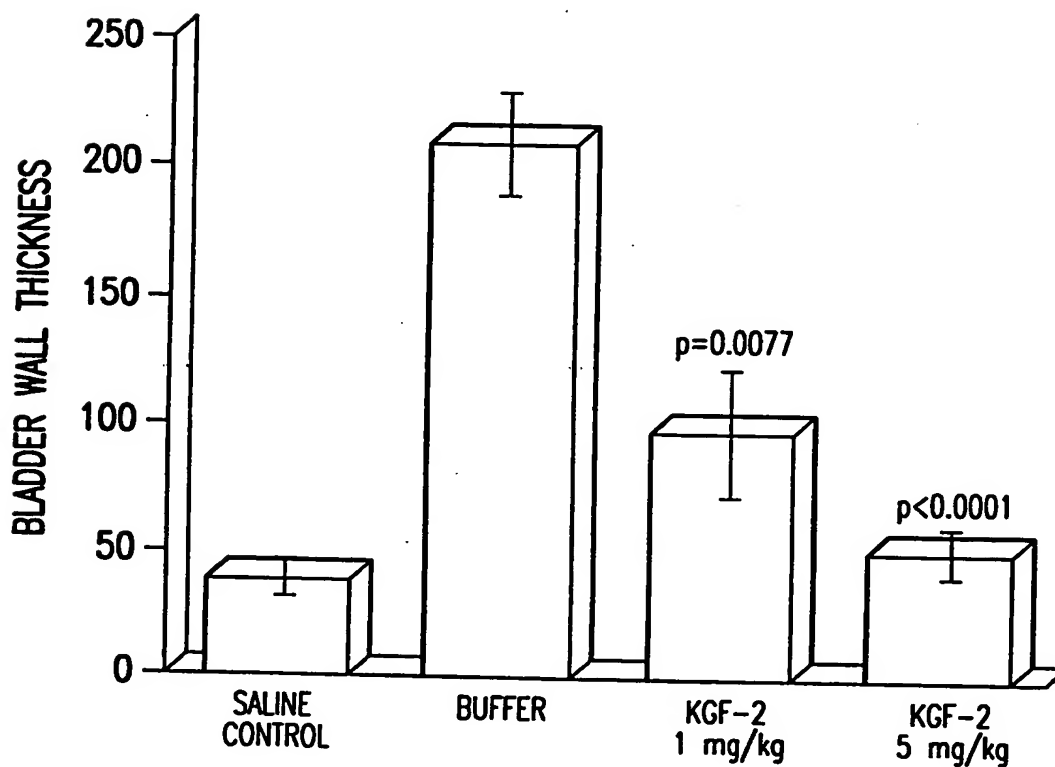


FIG. 55

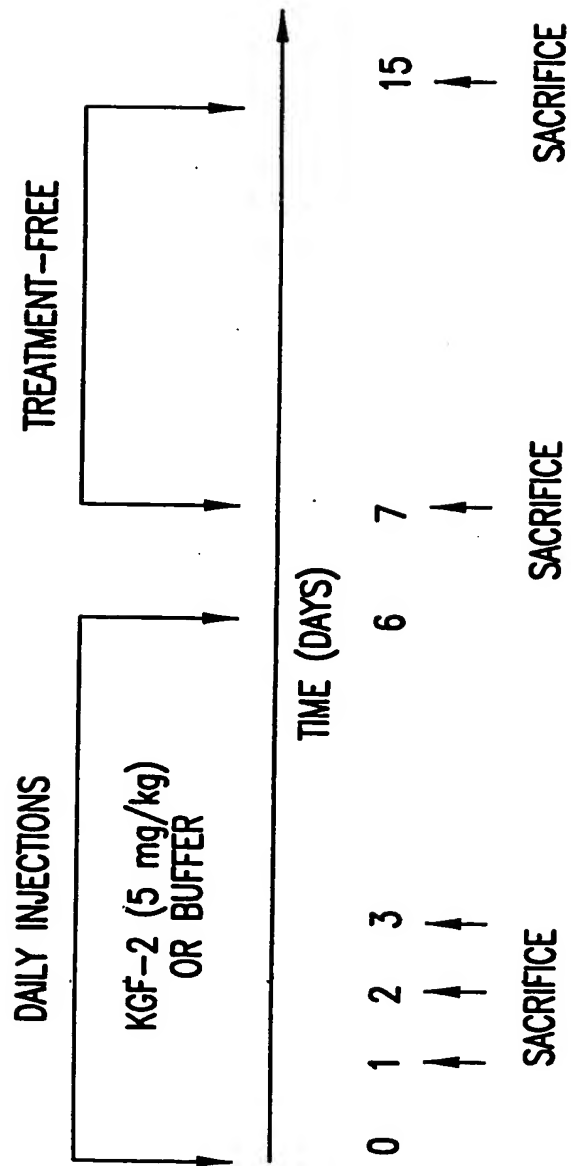


FIG. 56

PROLIFERATION OF HEPATOCYTES FOLLOWING SYSTEMIC ADMINISTRATION OF KGF-2

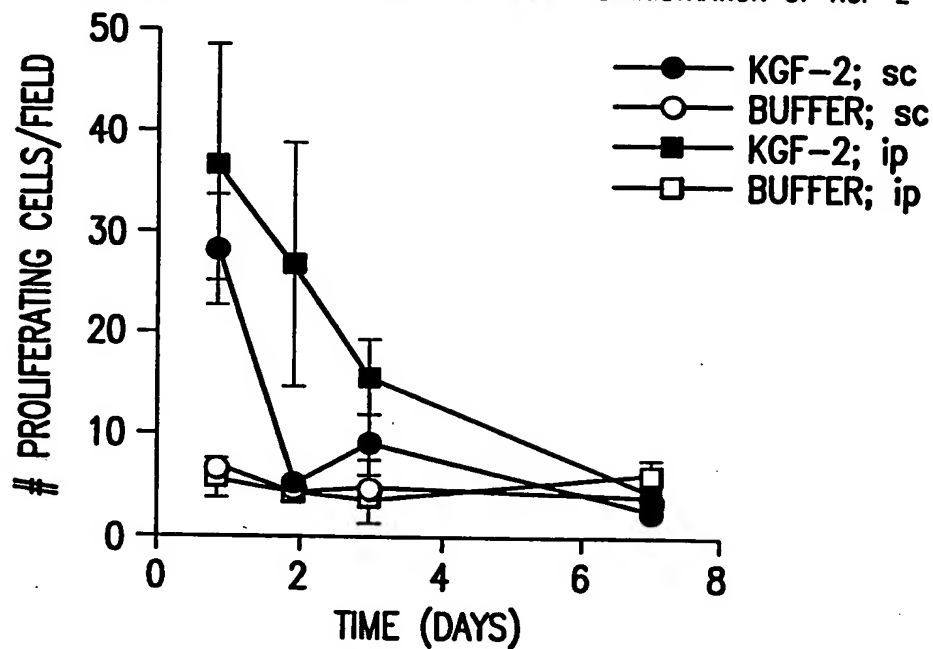


FIG. 57

PROLIFERATION OF PANCREATIC CELLS FOLLOWING SYSTEMIC ADMINISTRATION OF KGF-2

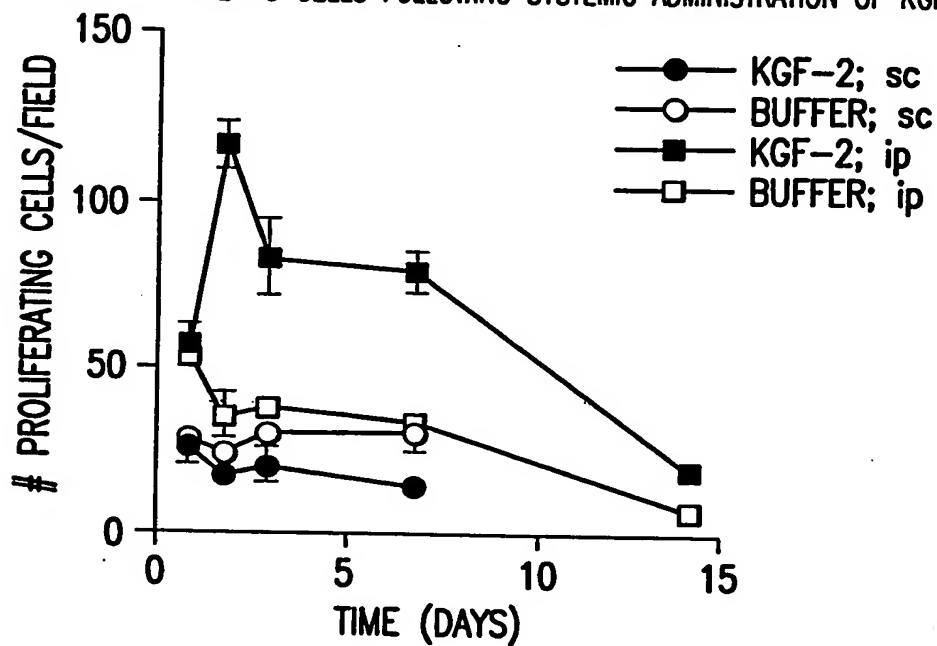


FIG. 58

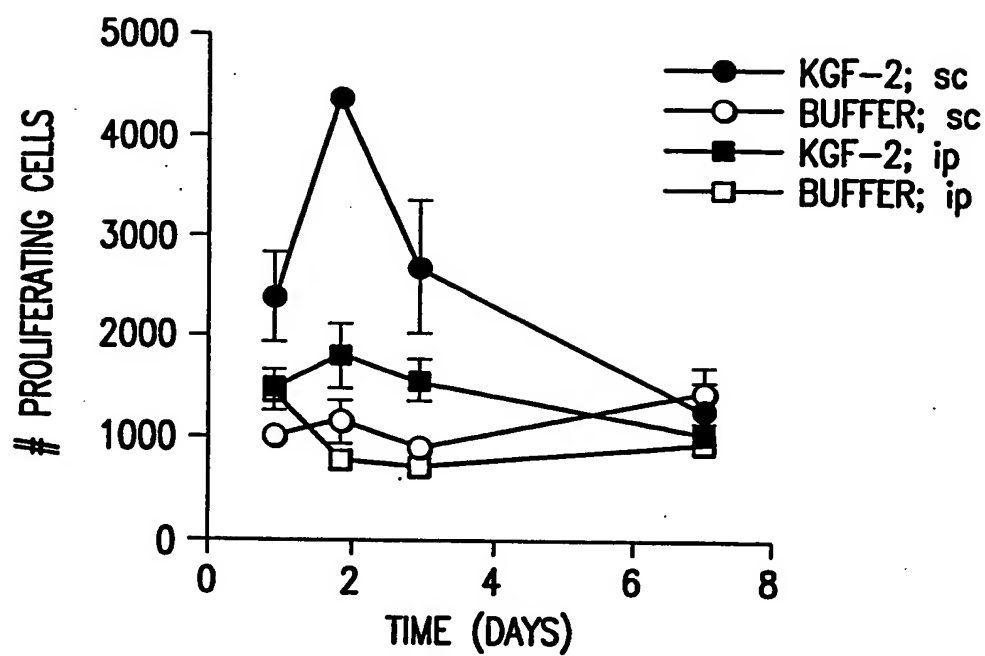


FIG. 59

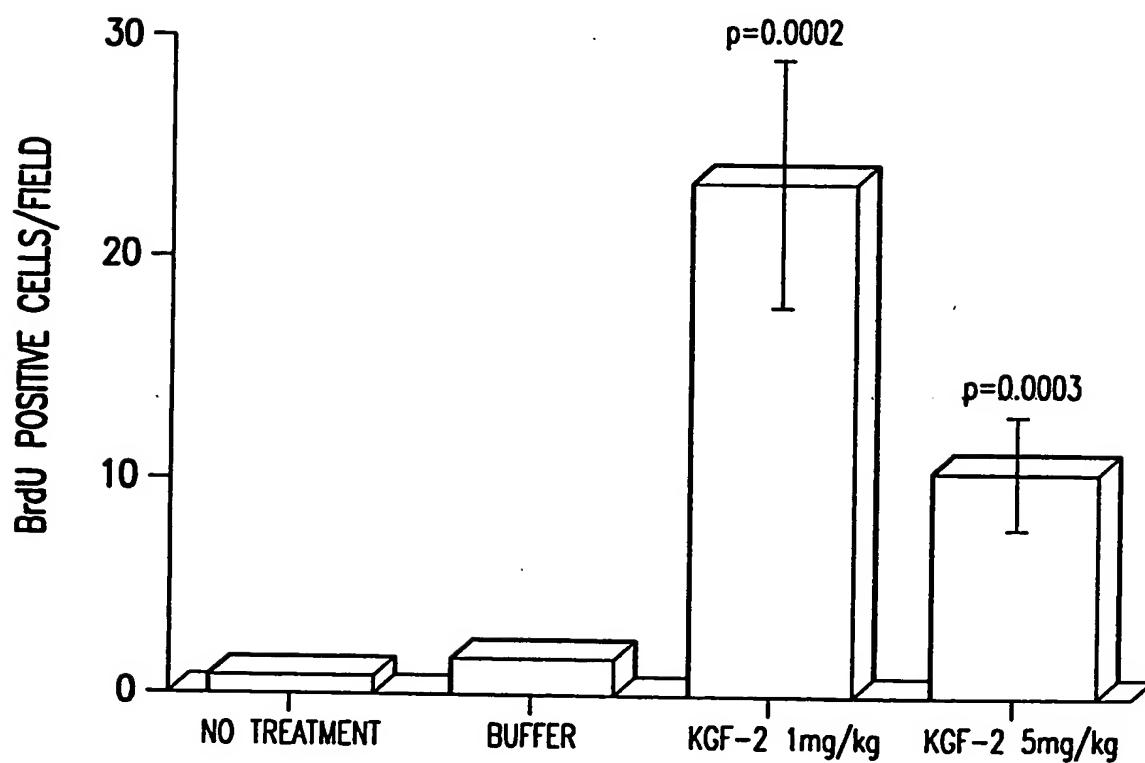


FIG. 60